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OM nucleic - nucleic search, using sw model
Run on: March 5, 2006, 10:17:20 ; Search time 824 Seconds
(without alignments)
8259.342 Million cell updates/sec

Title: US-10-660-208-90
Perfect score: 823
Sequence: 1 ctgacggtactccaagat.....cgatccattctccagcgag 823

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubnpa/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubnpa/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubnpa/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubnpa/US09B_PUBCOMB.seq.*
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8: /cgn2_6/ptodata/1/pubnpa/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubnpa/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubnpa/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	823	100.0	823	3	US-09-846-903-90
2	823	100.0	823	7	US-10-660-208-90
3	564	68.5	1587	3	US-09-846-903-87
4	564	68.5	1587	7	US-10-660-208-87
5	231	28.1	1578	7	US-10-425-114-22826
6	229	27.8	651	8	US-10-425-115-18768
7	220.2	26.8	1326	7	US-10-425-114-31817
8	220.2	26.8	2760	8	US-10-425-115-69837
9	209.2	25.4	6550	7	US-10-759-602-15
10	209.2	25.4	9299	7	US-10-759-602-16
11	209.2	25.4	9408	7	US-10-759-602-16
12	179.6	21.8	814	8	US-10-425-115-134827
13	179.4	21.8	485	7	US-10-425-114-23949
14	177.8	21.6	379	8	US-10-425-115-34629
15	143.2	17.4	443	8	US-10-425-115-57384
16	127.4	15.5	1014	8	US-10-425-115-145839
17	123.2	15.0	1088	8	US-10-739-930-2967
18	123	14.9	812	8	US-10-425-115-74208
19	113.4	13.8	802	8	US-10-425-115-36797
20	110.2	13.4	720	3	US-09-950-933A-8
21	99.4	12.1	460	8	US-10-425-115-60268
22	99.2	12.1	737	7	US-10-425-114-27876
23	84.6	10.3	521	8	US-10-425-115-24447

24	76.2	9.3	694	8	US-10-425-115-78019	Sequence 78019, A
25	75.6	9.2	1251	8	US-10-425-115-13680	Sequence 13680, A
26	75.2	9.1	875	8	US-10-425-115-13667	Sequence 13667, A
27	73	8.9	859	8	US-10-425-115-13670	Sequence 13670, A
28	71.4	8.7	836	8	US-10-425-115-13673	Sequence 13673, A
29	66	8.0	894	8	US-10-425-115-13677	Sequence 13677, A
30	63.4	7.7	270	8	US-10-425-115-145027	Sequence 145027, A
31	63.4	7.7	656	8	US-10-425-115-118219	Sequence 118219, A
32	62	7.5	821	7	US-10-425-114-16472	Sequence 16472, A
33	60	7.3	1696	7	US-10-425-114-32541	Sequence 32541, A
34	60	7.3	1979	8	US-10-425-115-144244	Sequence 144244, A
35	59.4	7.2	178	8	US-10-425-115-39694	Sequence 39694, A
36	59.2	7.2	833	8	US-10-425-115-54125	Sequence 54125, A
37	59	7.2	791	7	US-10-425-114-12914	Sequence 12914, A
38	59	7.2	795	7	US-10-425-114-12891	Sequence 12891, A
39	57.2	7.0	686	8	US-10-425-115-2162	Sequence 2162, Ap
40	56.8	6.9	783	8	US-10-425-115-44746	Sequence 44746, A
41	56.8	6.9	785	7	US-10-425-114-14246	Sequence 14246, A
42	56.8	6.9	877	8	US-10-425-115-44748	Sequence 44748, A
43	56.8	6.9	2404	8	US-10-425-115-40488	Sequence 40488, A
44	53.6	6.5	1090	7	US-10-425-114-24775	Sequence 24775, A
45	53.6	6.5	1140	8	US-10-425-115-132031	Sequence 132031, A

ALIGNMENTS

RESULT 1
US-09-846-903-90
Sequence 90, Application US/09846903
Publication No. US20030200565A1
GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Dubois, Patrice
APPLICANT: Malven, Marianne
APPLICANT: Masucci, James D.
TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
TITLE OF INVENTION: OF GENE EXPRESSION
FILE REFERENCE: 38-21(15678)B promoters
CURRENT APPLICATION NUMBER: US/09/846,903
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US 60/201,255
PRIOR FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 90
LENGTH: 823
TYPE: DNA
ORGANISM: Zea mays
US-09-846-903-90

Query Match	100.0%	Score 823, DB 3, Length 823;
Best Local Similarity	100.0%	Pred. No. 1.5e+239, Indels 0; Gaps 0;
Matches 823;	Conservative 0;	Mismatches 0;
Qy	1	CTGCACCGGTACTTCCAAAGTATAAGACACAGCTAAACACACATATGCGTGGTCAATGC 60
Db	1	CTGCACCGGTACTTCCAAAGTATAAGACACAGCTAAACACACATATGCGTGGTCAATGC 60
Qy	61	TAAACATGCTGCTTACCATATTCATTCATTCAGACATTCATTAATTAAGTGA 120
Db	61	TAAACATGCTGCTTACCATATTCATTCATTCAGACATTCATTAATTAAGTGA 120
Qy	121	CCATTCAGATGCTCTCTGTCGCCGAATATAGAGCTTAAGACACTGTCTTCGTCAGGATA 180
Db	121	CCATTCAGATGCTCTCTGTCGCCGAATATAGAGCTTAAGACACTGTCTTCGTCAGGATA 180
Qy	181	CATGCTTTGAGATTTTTCATTCATTCACCCCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
Db	181	CATGCTTTGAGATTTTTCATTCATTCACCCCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
Qy	241	ACCATTTGATACGTCCTTAACCTGCGACCGCTACCTAGGGGCTATTCAAGAACCAACCATG 300

241 ACCAATTGACATGCCCTAACTGGCACCGCTAGCTAGGGGCTATTCAAGAACCAACCATG 300
301 TACAGTTGTGCAACGCTGAATGGTTATTGCTTCAGATTAAAGCTTAATATTAGACTGA 360
301 TACAGTTGTGCAACGCTGAATGGTTATTGCTTCAGATTAAAGCTTAATATTAGACTGA 360
361 TGCAGCTCAATTCATAGACACAAACACAGTGTAGAGCCGCTATAGCAATTAAGCAACA 420
361 TGCAGCTCAATTCATAGACACAAACACAGTGTAGAGCCGCTATAGCAATTAAGCAACA 420
421 AGCGAATTCGTTAGCTACAAACCAATTTGCTGGGCTTCCATGGGCATCGCAGAAGTATT 480
421 AGCGAATTCGTTAGCTACAAACCAATTTGCTGGGCTTCCATGGGCATCGCAGAAGTATT 480
481 GTGGCTGATATTGCTGAATTAAGCGAGGCGCCCAAGGCGCCATCACTTCCTCGAGGT 540
481 GTGGCTGATATTGCTGAATTAAGCGAGGCGCCCAAGGCGCCATCACTTCCTCGAGGT 540
541 CAGCAATTCGTTAGCTACAAACCAATTTGCTGGGCTTCCATGGGCATCGCAGAAGTATT 600
541 CAGCAATTCGTTAGCTACAAACCAATTTGCTGGGCTTCCATGGGCATCGCAGAAGTATT 600
601 TTCTGGTTCAGTCAACATGCTCGATCCAGGGGCGGAGGAGCAACATGTTGGGCC 660
601 TTCTGGTTCAGTCAACATGCTCGATCCAGGGGCGGAGGAGCAACATGTTGGGCC 660
661 GCCGAGTGAGCCCAAGCGGAGCGCGTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 720
661 GCCGAGTGAGCCCAAGCGGAGCGCGTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 720
721 ATATACACAGCGCAGCATACCCATATCGTGTGCTAGAGCACTGAAACACAGCCGAGC 780
721 ATATACACAGCGCAGCATACCCATATCGTGTGCTAGAGCACTGAAACACAGCCGAGC 780
781 GATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGCAG 823
781 GATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGCAG 823

RESULT 2
US-10-660-208-90
; Sequence 90, Application US/10660208
; Publication No. US20040133946A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; FILE REFERENCE: 38-21(15678)B promoters
; CURRENT APPLICATION NUMBER: US/10/660,208
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 60/201,255
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 90
; LENGTH: 823
; TYPE: DNA
; ORGANISM: Zea mays

US-10-660-208-90

Query Match 100.0%; Score 823; DB 7; Length 823;
Best Local Similarity 100.0%; Pred. No. 1.5e-239;
Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGCAAGTACTCCAGTATAGACACACTAAACACACACATATGAGTGGTGTATGTC 60
1 CTGCAAGTACTCCAGTATAGACACACTAAACACACACATATGAGTGGTGTATGTC 60
61 TAAACATGTGCTTACCATATTTCATGTTATCAATCAGAACATTTCAATAAATTAAGTGA 120

61 TAAACATGTGCTTACCATATTTCATGTTATCAATCAGAACATTTCAATAAATTAAGTGA 120
121 CCATCAGATAGTCTCTCTGCCCCGATATAGAGCTAAGACACTGTGTCTTCGTCGAAGATA 180
121 CCATCAGATAGTCTCTCTGCCCCGATATAGAGCTAAGACACTGTGTCTTCGTCGAAGATA 180
181 CATGCTTTGAGATTTTTCATTTACATTTACCCCCCTAGACACACTCTTAAGACACAACCTTAAGAC 240
181 CATGCTTTGAGATTTTTCATTTACATTTACCCCCCTAGACACACTCTTAAGACACAACCTTAAGAC 240
241 ACCATTTGATACATGCTTAACTGCGCACCGCTAGTAGGGGCTATTCAAGAACCAACCATG 300
241 ACCATTTGATACATGCTTAACTGCGCACCGCTAGTAGGGGCTATTCAAGAACCAACCATG 300
301 TACAGTTGTTGCAACGTTGAATGTTATTGCTTCAGATTAAAGCTAATTTTAGACTGA 360
301 TACAGTTGTTGCAACGTTGAATGTTATTGCTTCAGATTAAAGCTAATTTTAGACTGA 360
361 TGCAGCTGCAATTCATAGACACAAACACAGTGTAGAGCCGCTATAGCAATTAAGCAACA 420
361 TGCAGCTGCAATTCATAGACACAAACACAGTGTAGAGCCGCTATAGCAATTAAGCAACA 420
421 AGCGAATTCGTTAGCTACAAACCAATTTGCTGGGCTTCCATGGGCATCGCAGAAGTATT 480
421 AGCGAATTCGTTAGCTACAAACCAATTTGCTGGGCTTCCATGGGCATCGCAGAAGTATT 480
481 GTGGCTGATATTGCTGAATTAAGCGAGGCGCCCAAGGCGCCATCACTTCCTCGAGGT 540
481 GTGGCTGATATTGCTGAATTAAGCGAGGCGCCCAAGGCGCCATCACTTCCTCGAGGT 540
541 CAGCAATTCGTTAGCTACAAACCAATTTGCTGGGCTTCCATGGGCATCGCAGAAGTATT 600
541 CAGCAATTCGTTAGCTACAAACCAATTTGCTGGGCTTCCATGGGCATCGCAGAAGTATT 600
601 TTCTGGTTCAGTCAACATGCTCGATCCAGGGGCGGAGGAGCAACATGTTGGGCC 660
601 TTCTGGTTCAGTCAACATGCTCGATCCAGGGGCGGAGGAGCAACATGTTGGGCC 660
661 GCCGAGTGAGCCCAAGCGGAGCGCGTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 720
661 GCCGAGTGAGCCCAAGCGGAGCGCGTCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 720
721 ATATACACAGCGCAGCATACCCATATCGTGTGCTAGAGCACTGAAACACAGCCGAGC 780
721 ATATACACAGCGCAGCATACCCATATCGTGTGCTAGAGCACTGAAACACAGCCGAGC 780
781 GATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGCAG 823
781 GATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGCAG 823

RESULT 3
US-09-846-903-87
; Sequence 87, Application US/09846903
; Publication No. US20030200565A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; FILE REFERENCE: 38-21(15678)B promoters
; CURRENT APPLICATION NUMBER: US/09/846,903
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/201,255
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 87
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Zea mays

US-09-846-903-87

Query Match 68.5%; Score 564; DB 3; Length 1587;
Best Local Similarity 99.1%; Pred. No. 1.8e-160;
Matches 567; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 252 ATGCCCTAACTGGCAGCGCTACGTAGGGGCTATTCAAGAACCAACCAATGTACAGTTGTTG 311
DB 992 ATGGCTTAACTGGCAGCGCTACGTAGGGGCTATTCAAGAACCAACCAATGTACAGTTGTTG 1051

QY 312 CAACGTGAATGGTTATTGCTTTCAGATTAAAGCTAAATTTATTAGACTGATGCGAGTCAAA 371
DB 1052 CAACGTGAATGGTTATTGCTTTCAGATTAAAGCTAAATTTATTAGACTGATGCGAGTCAAA 1111

QY 372 TTCCATAGAGACAAAACAGTGTAGAACCGCTATAGCAATTAAGCAACCAAGCGAACATTG 431
DB 1112 TTCCATAGAGACAAAACAGTGTAGAACCGCTATAGCAATTAAGCAACCAAGCGAACATTG 1171

QY 432 CTTAGCTACAACTAATTTGCTGGGCTTCCATGGGCATCGCAGAAAGTATTGTGGCTGCATA 491
DB 1172 CTTAGCTACAACTAATTTGCTGGGCTTCCATGGGCATCGCAGAAAGTATTGTGGCTGCATA 1231

QY 492 TTGCTGAAATTTATAGCAGGCGCCCAAGGCCCATCACTTCACTTAAATAGACCAAGTTGTTGTTCTA 551
DB 1232 TTGCTGAAATTTATAGCAGGCGCCCAAGGCCCATCACTTCACTTAAATAGACCAAGTTGTTGTTCTA 1291

QY 552 TTTTGTAACTGCTCGATTAATTTGTTTCACTTAAATAGACCAAGTTGTTGTTCTA 611
DB 1292 TTTTGTAACTGCTCGATTAATTTGTTTCACTTAAATAGACCAAGTTGTTGTTCTA 1351

QY 612 GTCAACATGCTCGATTAATTTGTTTCACTTAAATAGACCAAGTTGTTGTTCTA 671
DB 1352 GTCAACATGCTCGATTAATTTGTTTCACTTAAATAGACCAAGTTGTTGTTCTA 1411

QY 672 GTCAACATGCTCGATTAATTTGTTTCACTTAAATAGACCAAGTTGTTGTTCTA 731
DB 1412 GTCAACATGCTCGATTAATTTGTTTCACTTAAATAGACCAAGTTGTTGTTCTA 1471

QY 732 CGCAGATACCCATATCGTGGTGTAGAACCAACTGAAACAGCGGAGCGGATCTCTCTC 791
DB 1472 CGCAGATACCCATATCGTGGTGTAGAACCAACTGAAACAGCGGAGCGGATCTCTCTC 1531

QY 792 CCTCTCCCTCTCCGATCCATTTCCAGCGCAG 823
DB 1532 CCTCTCCCTCTCCGATCCATTTCCAGCGCAG 1563
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RESULT 4

US-10-660-208-87
; Sequence 87, Application US/10660208
; Publication No. US20040133948A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Maucucci, James D.
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; FILE REFERENCE: 38:21(15678)B promoters
; CURRENT APPLICATION NUMBER: US/10/660,208
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 60/201,255
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Zea mays

Query Match 68.5%; Score 564; DB 7; Length 1587;
Best Local Similarity 99.1%; Pred. No. 1.8e-160;

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Matches 567; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 252 ATGCCCTAACTGGCAGCGCTACGTAGGGGCTATTCAAGAACCAACCAATGTACAGTTGTTG 311
DB 992 ATGGCTTAACTGGCAGCGCTACGTAGGGGCTATTCAAGAACCAACCAATGTACAGTTGTTG 1051

QY 312 CAACGTGAATGGTTATTGCTTTCAGATTAAAGCTAAATTTATTAGACTGATGCGAGTCAAA 371
DB 1052 CAACGTGAATGGTTATTGCTTTCAGATTAAAGCTAAATTTATTAGACTGATGCGAGTCAAA 1111

QY 372 TTCCATAGAGACAAAACAGTGTAGAACCGCTATAGCAATTAAGCAACCAAGCGAACATTG 431
DB 1112 TTCCATAGAGACAAAACAGTGTAGAACCGCTATAGCAATTAAGCAACCAAGCGAACATTG 1171

QY 432 CTTAGCTACAACTAATTTGCTGGGCTTCCATGGGCATCGCAGAAAGTATTGTGGCTGCATA 491
DB 1172 CTTAGCTACAACTAATTTGCTGGGCTTCCATGGGCATCGCAGAAAGTATTGTGGCTGCATA 1231

QY 492 TTGCTGAAATTTATAGCAGGCGCCCAAGGCCCATCACTTCACTTAAATAGACCAAGTTGTTGTTCTA 551
DB 1232 TTGCTGAAATTTATAGCAGGCGCCCAAGGCCCATCACTTCACTTAAATAGACCAAGTTGTTGTTCTA 1291

QY 552 TTTTGTAACTGCTCGATTAATTTGTTTCACTTAAATAGACCAAGTTGTTGTTCTA 611
DB 1292 TTTTGTAACTGCTCGATTAATTTGTTTCACTTAAATAGACCAAGTTGTTGTTCTA 1351

QY 612 GTCAACATGCTCGATTAATTTGTTTCACTTAAATAGACCAAGTTGTTGTTCTA 671
DB 1352 GTCAACATGCTCGATTAATTTGTTTCACTTAAATAGACCAAGTTGTTGTTCTA 1411

QY 672 GTCAACATGCTCGATTAATTTGTTTCACTTAAATAGACCAAGTTGTTGTTCTA 731
DB 1412 GTCAACATGCTCGATTAATTTGTTTCACTTAAATAGACCAAGTTGTTGTTCTA 1471

QY 732 CGCAGATACCCATATCGTGGTGTAGAACCAACTGAAACAGCGGAGCGGATCTCTCTC 791
DB 1472 CGCAGATACCCATATCGTGGTGTAGAACCAACTGAAACAGCGGAGCGGATCTCTCTC 1531

QY 792 CCTCTCCCTCTCCGATCCATTTCCAGCGCAG 823
DB 1532 CCTCTCCCTCTCCGATCCATTTCCAGCGCAG 1563
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RESULT 5

US-10-425-114-22826/c
; Sequence 22826, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 22826
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: L1B3591-120-All_FLI
US-10-425-114-22826

Query Match 28.1%; Score 231; DB 7; Length 1578;
Best Local Similarity 92.4%; Pred. No. 5.2e-59;
Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 TGCACGGTACTCCAGTATAGACACAGCTAAACACAACTAATGCGTGGTGTCTCTCTC 61

Db 1054 TGCACGGTACTCCAAGTATAAGACACACTTAAACACACATATATACAGTGGAGTGTCT 995
Qy 62 AAAACATGTGCTTACCATATTTTATCATTAATCAGAACATTTCAATAAATTTAAAGTGAC 121
Db 994 AAAACATGTGCTTACCATATTTTATTTGTTACCAATCAGAGCATTTCAATAAATTTAAAGTGAC 935
Qy 122 CAATCAGATAGTCTCTGTCGGGAATATAGAGCTTAAGACACTGTGCTTCTGTCAGATAC 181
Db 934 CAATCAGCTAGTCTCATGCTCTCGAATAGAGCTTAAGACACTGTGCTTCTGTCAGATAC 875
Qy 182 ATGCTCTCAGATTTTATCATTTACCCCTAGACACACTCTTAAGACACAACTTTAAGACA 241
Db 874 ATATCTTGAGTTTTTTTACATTTACCCCTTAAGACACACTCGAAGACATTAATCTAAGACA 815
Qy 242 CCCATTGTACATGCCCTAACTGG 264
Db 814 CCCACTGTACATGCCCTAATCGG 792

RESULT 6
US-10-425-115-18768
; Sequence 18768, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 18768
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_117117C.1
US-10-425-115-18768

Query Match 27.8%; Score 229; DB 8; Length 651;
Best Local Similarity 92.3%; Pred. No. 1.3e-58;
Matches 241; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 1 CTGCACGGTACTCCAAGTATAAGACACAGCTAAACACACATATATGCAAGTGGTCAATGTC 60
Db 211 CTGCACGGTACTCCAAGTATAAGACACACACTTAACACATATATATACAGTGGTCAATGTC 270
Qy 61 TAAACATGTGCTTACCATATTTTATCATTAATCAGAACATTTCAATAAATTTAAAGTGA 120
Db 271 TAAATATGTGCTTACCATATTTTATTTGTTACCAATCAAGCATTTCAATAAATTTAAAGTGA 330
Qy 121 CAATCAGATAGTCTCTGTCGGGAATATAGAGCTTAAGACACTGTGCTTCTGTCAGATAC 180
Db 331 TCAATCAGCTAGTCTCTCTCTCGAATAGAGCTTAAGACACTGTGCTTCTGTCAGATAC 390
Qy 181 CATGCTTGTAGATTTTATCATTTACCCCTAGACACACTCTTAAGACACAACTTTAAGAC 240
Db 391 CATGCTTGTAGTTTTTTTACATTTACCCCTTAGACACACTCTTAAGACACAACTTTAAGAC 450
Qy 241 ACCATTGTACATGCCCTAACT 261
Db 451 ACCATTGTACATGCCCTTAC 471

RESULT 7
US-10-425-114-31817
; Sequence 31817, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:

; APPLICANT: Liu, Jingsong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 31817
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73222F10_FLI
US-10-425-114-31817

Query Match 26.8%; Score 220.2; DB 7; Length 1326;
Best Local Similarity 91.1%; Pred. No. 9.1e-56;
Matches 245; Conservative 0; Mismatches 23; Indels 1; Gaps 1;
Qy 1 CTGCACGGTACTCCAAGTATAAGACACAGCTAAACACACATATATGCAAGTGGTCAATGTC 60
Db 134 CTGCACGGTACTATAGTATAAGACACACTTAACACATATATATACAGTGGTCAATGTC 193
Qy 61 TAAACATGTGCTTACCATATTTTATCATTAATCAGAACATTTCAATAAATTTAAAGTGA 120
Db 194 TAAACATGTGCTTACCATATTTTATTTTACATTTCTTCAATCAGAGCATTTCAATAAATTTAAAGTGA 253
Qy 121 CAATCAGATAGTCTCTGTCGGGAATATAGAGCTTAAGACACTGTGCTTCTGTCAGATAC 180
Db 254 CCTATCAGTAGTCTCTGCTCTCAACATAGAGCTAAGACATTTGCTGCTTCTGTCAGATAC 313
Qy 181 CATGCTTGTAGATTTTATCATTTACCCCTAGACACACTCTTAAGACACAACTTTAAGAC 240
Db 314 CATGCTTGTAGTTTTTTTACATTTCA-CCCTTAGACACACTTTTAAGACACAACTTTAAGAC 372
Qy 241 ACCATTGTACATGCCCTAACTGACCG 269
Db 373 ACATATTGTACATGCCCTTAAGGGAGTGC 401

RESULT 8
US-10-425-115-69837/c
; Sequence 69837, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 69837
; LENGTH: 2760
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_163683C.1
US-10-425-115-69837

Query Match 26.8%; Score 220.2; DB 8; Length 2760;
Best Local Similarity 91.1%; Pred. No. 1.4e-55;
Matches 245; Conservative 0; Mismatches 23; Indels 1; Gaps 1;
Qy 1 CTGCACGGTACTCCAAGTATAAGACACAGCTAAACACACATATATGCAAGTGGTCAATGTC 60

	Query Match	25.4%	Score 209.2	DB 7	Length 9408
	Best Local Similarity	90.1%	Pred. No. 6.1e-52		
	Matches 236	Conservative 0	Mismatches 23	Indels 3	Gaps 1
Qy	2	TCGACGGTACTCCAAGTATATAGACACACAGCTAAACACACAATAATG---	CGTGGTCATG	58	
Db	1408	TGCACAGTACTCCAAGTATATAGACACACACTTAAACACACAATAATAATACAGCTGTTATA	1467		
Qy	59	TCTAAACAATGTGCTTACCATATTCATGTATCAATCAGAACATTCATATAAATTTAAAGT	118		
Db	1468	TCTAAACAATGTGCTTACCATATTCATGTACCAATTTAGAACATTTAATAAATTTAAAGT	1527		
Qy	119	GACCAATCAGATAGTCTCCTGTCCGAATATAGAGCTTAAGACACATGTGCTCTTCGTCGAAGA	178		

Query Match	21.8%	Score 179.6	DB 8	Length 814
Best Local Similarity	93.1%	Pred. No. 1.6e-43		
Matches 188	Conservative	0	Mismatches 14	Indels 0
Gap8	0			
QY	59	TCATAAACATGCTCTTACCATATTCATTGTATCAATCAGAACAATTCAAATAAATTTAAAGT	118	
DB	814	TGTCATAAACATGCTCTTATCATATTCATTGTACCAATCAAACAATTCAAATAAATTTAAAGT	755	
QY	119	GACCAATTCAGATAGTCTCCTGTCTCCGATATATAGCTTAAGCACTGTGCTTCGTCGAAGA	178	
DB	754	GACCAATTCAGATAGTCTCCTTTTCTCGAATATAGAGCTTAAGCACTGTGCTTCGTCGAAGA	695	
QY	179	TACATGCTCTTGAGATTTTTTATCAATTCACCCCCCTTAGACACACTCTTAAGACACAACACTTTAAG	238	
DB	694	TAGTGTCTTGAGATTTTTTATCAATTCACCCCCCTTAGACACACTCTTAAGACACAACACTTTAAG	635	
QY	239	ACACCCATTGTACATGCCCTTAA	260	
DB	634	ACACCCACTGTACATGCCCTTA	613	

RESULT 13
 US-10-425-114-23949/c
 ; Sequence 23949, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 23949

LENGTH: 485
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3606-031-G10_FLI
US-10-425-114-23949

Query Match 21.6%; Score 179.4; DB 7; Length 485;
Best Local Similarity 94.4%; Pred. No. 1.4e-43;
Matches 186; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 64 AACATGTCCTTACCATATTCATTCATCAATCAGAACATTCATCAATTAAGTGACCA 123
Db 481 AAACATGTCCTTATCATATTCATTCATCAATCAAAACATTCATCAATTAAGTGACCA 422

Qy 124 ATCAGATAGTCCTCTGTCCTCCCAATATAGAGCTAGACACTGTCTCTCGTCAAGATACAT 183
Db 421 ATCAGATAGTCCTCTGTCCTCCCAATATAGAGCTAGACACTGTCTCTCGTCAAGATACAT 362

Qy 184 GTCTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGACACC 243
Db 361 GTCTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGACACC 302

Qy 244 CATGTACATGCCCTAA 260
Db 301 CACTGTACATGCCCTTA 285

RESULT 14
US-10-425-115-34629/c
Sequence 34629, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 34629
LENGTH: 379
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1) (379)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_131586C.1
US-10-425-115-34629

Query Match 21.6%; Score 177.8; DB 8; Length 379;
Best Local Similarity 86.3%; Pred. No. 3.8e-43;
Matches 208; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

Qy 25 CACAGCTAAACACACATATGAGTGGTGTCTGCTAAACATGTCCTTACCATATTC 84
Db 379 CATAACTAAACACACAT 320

Qy 85 ATTGTATCAATCAGAACATTCATTAATTAAGTGACCAATCAGATAGTCCTCTGTCCTCG 144
Db 319 ATTATACAAATCAGAGCACTTCAATTAATTAAGTGATCAATCAAAATATCTACTGTCTCG 260

Qy 145 AATATAGAGCTAAGACACTGTCTCTGTCAGATACATGTCCTGAGATTTTACATTC 204
Db 259 AACATAGAGCTAAGACACTGTCTCTGTCAGATACATGTCCTGAGTCTTTTAAACATTT 200

Qy 205 ACCCCCTAGACACACTCTTAAGACACAACTTAAAGACACCCATTTGATACATGCCCTAACTGG 264

Db 199 A-CCCCCTAGACATACCTACCCCAACAACTTAAACAACTCACTGTATCATGCCATAACGGT 141

Qy 265 C 265

Db 140 C 140

RESULT 15
US-10-425-115-57384
Sequence 57384, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 57384
LENGTH: 443
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_152328C.1
US-10-425-115-57384

Query Match 17.4%; Score 143.2; DB 8; Length 443;
Best Local Similarity 79.7%; Pred. No. 1.4e-32;
Matches 169; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 62 AAAACATGTCCTTACCATATTCATTCATCAATCAGAACATTCATCAATTAAGTGAC 121
Db 7 AAACATGTCCTTACCATATTCATTCATCAATCAGAACATTCATCAATTAAGTGAC 66

Qy 122 CAATCAGATAGTCCTCTGTCCTCCGAATATAGAGCTAGACACTGTCTCTGTCAGATAC 181
Db 67 CAATCAGCTAGCTCTCTGTCCTCAATTTGAGCTAAACACTGGTTTTCGGAATAATAC 126

Qy 182 ATGTCTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAAGACA 241
Db 127 ATGTCTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAAGACA 186

Qy 242 CCATTTGATACATGCCCTTAACTGGCAGCGCTAC 273
Db 187 CCCACTGTATGCTGCTGACAGGGGCCAAAC 218

Search completed: March 5, 2006, 11:26:21
Job time : 825 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 11:08:25 ; Search time 513 Seconds
(without alignments)
3517.379 Million cell updates/sec

Title: US-10-660-208-90

Perfect score: 823

Sequence: 1 ctgcacgtactcaagtat.....cgatccattccagcgag 823

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:

- 1: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	44.6	5.4	393323	7 US-10-330-773-23	Sequence 23, Appl
C 2	37.4	4.5	2010	6 US-09-925-065A-715737	Sequence 715737
C 3	37.4	4.5	2010	6 US-09-925-065A-715738	Sequence 715738
C 4	37.4	4.5	2010	6 US-09-925-065A-715739	Sequence 715739
C 5	36.4	4.4	1148	6 US-09-925-065A-717296	Sequence 717296
C 6	36	4.4	415	6 US-09-925-065A-652867	Sequence 652867
C 7	36	4.4	1829	8 US-10-750-185-64389	Sequence 64389, A
C 8	36	4.4	1829	8 US-10-750-623-64389	Sequence 64389, A
C 9	36	4.4	4149	12 US-11-098-686-9452	Sequence 9452, Ap
C 10	36	4.4	1457619	12 US-11-098-686-8739	Sequence 8739, Ap
C 11	34.8	4.2	904	6 US-09-925-065A-3542	Sequence 3542, Ap
C 12	34.8	4.2	523643	7 US-10-330-773-308	Sequence 308, Appl
C 13	34.6	4.2	509	6 US-09-925-065A-630175	Sequence 630175
C 14	34.6	4.2	529	6 US-09-925-065A-192068	Sequence 192068
C 15	34.2	4.2	419	6 US-09-925-065A-487029	Sequence 487029
C 16	34.2	4.2	419	6 US-09-925-065A-487030	Sequence 487030
C 17	33.8	4.1	523643	7 US-10-330-773-308	Sequence 308, Appl
C 18	33.6	4.1	1784	6 US-09-925-065A-671953	Sequence 671953
C 19	33.6	4.1	2759	8 US-10-750-185-34470	Sequence 34470, A
C 20	33.6	4.1	2759	8 US-10-750-623-34470	Sequence 34470, A

C 21	33.6	4.1	6433	7 US-10-330-773-711	Sequence 711, App
C 22	33.6	4.1	121167	7 US-10-330-773-710	Sequence 710, App
C 23	33.4	4.1	521	6 US-09-925-065A-140955	Sequence 140955
C 24	33.4	4.1	540	6 US-09-925-065A-111937	Sequence 111937
C 25	33.2	4.0	459	6 US-09-925-065A-199187	Sequence 199187
C 26	33.2	4.0	536	6 US-09-925-065A-333591	Sequence 333591
C 27	33.2	4.0	551	6 US-09-925-065A-447145	Sequence 447145
C 28	33.2	4.0	560	6 US-09-925-065A-190696	Sequence 190696
C 29	33.2	4.0	573	6 US-09-925-065A-784400	Sequence 784400
C 30	33.2	4.0	618	6 US-09-925-065A-402539	Sequence 402539
C 31	33.2	4.0	615	6 US-09-925-065A-169134	Sequence 169134
C 32	33.2	4.0	640	6 US-09-925-065A-783578	Sequence 783578
C 33	33.2	4.0	1220	6 US-09-925-065A-690610	Sequence 690610
C 34	33.2	4.0	2100	6 US-09-925-065A-720567	Sequence 720567
C 35	33.2	4.0	254396	7 US-10-330-773-534	Sequence 534, App
C 36	33	4.0	388	6 US-09-925-065A-393782	Sequence 393782
C 37	33	4.0	512	6 US-09-925-065A-499969	Sequence 499969
C 38	33	4.0	529	6 US-09-925-065A-192067	Sequence 192067
C 39	33	4.0	588	6 US-09-925-065A-249129	Sequence 249129
C 40	33	4.0	776	6 US-09-925-065A-711775	Sequence 711775
C 41	33	4.0	1020	8 US-10-750-185-49985	Sequence 49985, A
C 42	33	4.0	1020	8 US-10-750-623-49985	Sequence 49985, A
C 43	33	4.0	1272	8 US-10-750-185-51144	Sequence 51144, A
C 44	33	4.0	1272	8 US-10-750-623-51144	Sequence 51144, A
C 45	33	4.0	8537	8 US-10-340-708-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-10-330-773-23/c
; Sequence 23, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 393323
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(393323)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-23

Query Match 5.4%; Score 44.6; DB 7; Length 393323;
Best Local Similarity 46.3%; Pred. No. 0.46;
Matches 146; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
QY 112 TTAAAGTGACCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAGACACTGTGTCTTC 171
DB 160000 TCAATGGTCTGTTACATAATATCAAGGTCTTATTTAACTGGGCATATATCTATGAATA 159941
QY 172 GTCAAGATACATGCTCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACA 231
DB 159940 TGTATAGTAGTGTGTTTAAATATTAATAACACACACACACACACACACACACA 159881
QY 232 ACTTAAGACACCACTTGTATACATGCCCTAATCTGCACCGCTACGTAGGGGCTATTCAAGAA 291
DB 159880 CACACACACACACACTTCTTATGGAAATATATGATGGCTACCTTCAGCTGAAGGAAA 159821
QY 292 CCAACCATGTACAGTTGTTGCAACGTGAATGTTATTTGCTTCAGATTAAGCTAATTAT 351
DB 159820 GAGATTTCTTCCACTATATAGCAACATCCAAGATGCTTGGTTTAAAAAATAAATAACAAG 159761

RESULT 7
US-10-750-185-64389
; Sequence 64389, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64389
; LENGTH: 1829
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-64389

Query Match	4.4%;	Score 36;	DB 8;	Length 1829;
Best Local Similarity	50.0%;	Pred. No. 11;		
Matches 90;	Conservative 0;	Mismatches 90;	Indels 0;	Gaps 0;

QY	294	AACCATGTACAGTTGTGCAACGTGAATGGTTATTGCTTCACATTAAAGCTAATTATTT	353
Db	942	AACTGTATTAACTGTTGAAGCTTTTAATTTTCATTACTTTAATGGGAATTATGAACCTT	1001
QY	354	AGACTGTATCAGCTGCAATTTCATAGAGACAAACACAGTGTGAAGCGCGTATAAGCATATAA	413
Db	1002	AGAACTATTTTGAAGCAAGTATTTCATATAAACATCACAGAATAAGCCCTTGTATTATA	1061
QY	414	GCAACAACAGCGAAACATTGCTTAGCTACAAACCAATTTGCTGGGCTTCATCGGGCATCGCAG	473
Db	1062	GTACACCAAGTCATGTCGATTTCTTTGACCCCATGGCTCCTCTGTGTCATGGAAATTCAG	1121

RESULT 8
US-10-750-623-64389


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; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3542
; LENGTH: 904
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-3542

Query Match      4.2%; Score 34.8; DB 6; Length 904;
Best Local Similarity 51.3%; Pred. No. 18;
Matches 81; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 282 TATTCAAGAACCAACCATGTACAGTGTGCAACGTGAATGGTTATTTGCTTCAGATTAA 341
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Db 311 TATTCATATGACCAACATATTTATTCAGAGTCCCTATATTTTCAGAGTGGCTAT 370
    |||||
QY 342 AGCTAATATTTAGACTGATGAGTCAATTCATAGACAAACAAACAGTGTAGAAGCCG 401
    |||||
Db 371 AGCAAGGGAGTGCACCAACCATTTTGTATTTGGCAGAGACTCAACACATGTCAGGGGAG 430
    |||||
QY 402 TATAAGCATTAAAGCAACGACGACATTTGCTTAGCTA 439
    |||||
Db 431 TGGAAACATTTTGTATTGAAAGGAAAGGCTCAGGTA 468
    |||||

RESULT 12
US-10-330-773-308
; Sequence 308, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 523643
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)...(523643)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-308

Query Match      4.2%; Score 34.8; DB 7; Length 523643;
Best Local Similarity 52.0%; Pred. No. 2.5e+02;
Matches 78; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 10 ACTCCAAGTATATACACACAGCTAAAAACACAAATAATGACGTGGTCAATGCTAAAAACATG 69
    |||||
Db 40005 AATAGAAGTGTAAATACATACATAACAAAGCAGAAAAAGGAAGTCACTATCTTTAAAGATG 40064
    |||||
QY 70 TGCTTACCATATTCATTTGTATCAATCAGAACATTCATTAATTAAGTGACCAATCAGA 129
    |||||
Db 40065 TTTTATTTTAAATAATTTTATTTATGAAGAATTATAAAACCTAATAAAGATGCTCTCA 40124
    |||||
QY 130 TAGTCTCTCTGCCGAATATAGAGCTAAGA 159
    |||||
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Db 40125 TATGTACCTTCATCATCTCTCTTTAATA 40154
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RESULT 13
US-09-925-065A-630175/c
; Sequence 630175, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 630175
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-630175

Query Match      4.2%; Score 34.6; DB 6; Length 509;
Best Local Similarity 45.9%; Pred. No. 16;
Matches 150; Conservative 1; Mismatches 175; Indels 1; Gaps 1;

QY 12 TCCAAGTATACACACAGCTTAAACACACATATTCAGTGGTCAATGCTTAAACATGTG 71
    |||||
Db 441 TTTATTAACAGGACCAAGAGCATTCACATAAAGAAATATTGCGAATTTGGATTTAATA 382
    |||||
QY 72 TCTTACCATATTCATTGTATCAATCAGAACATTTCAATAAATTAAGTGACCAATCAGATA 131
    |||||
Db 381 TATTGTAACTTCTGTTTCATCAAAAAGTACACAAAAGAAATATAAAGGAAACCCACAGA 322
    |||||
QY 132 GTCTCTCTGTCGGAATATAGAGCTAAGACACTGTGTTGTCGTCGAAGATACATGCTTTGAG 191
    |||||
Db 321 TTGAGATATCTGTCTATATGTAGACCTGACAAAGAACTATTATGACAGTATATATATA 262
    |||||
QY 192 ATTTTTCATTTACCCCTAGACACACTCTAAGACACACTTAAGACACACCACTTAAGACACCA 250
    |||||
Db 261 TATATATATATATATACACACACACACATATATATATATATATATATATACACACATATA 202
    |||||
QY 251 CATGCCCTAACTGGACCCCTAGTAGGGGCTATTCAAGAACCAACCATGTACAGTTGTT 310
    |||||
Db 201 TACACACACACACACACCCCTATACGCTGGCAATCAATAGAAAGAAAGTAAACATAT 142
    |||||
QY 311 GCAACGTGAATGTTTATTGCTTCAGA 337
    |||||
Db 141 TCAATTTTAAACCAAAATTTTAAACAGA 115
    |||||

RESULT 14
US-09-925-065A-192068
; Sequence 192068, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 08:22:14 ; Search time 275 Seconds
(without alignments)
5319.757 Million cell updates/sec

Title: US-10-660-208-90

Perfect score: 823

Sequence: 1 ctgcagtgactcgaagtat.....cgatccattctccagcgag 823

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	27.6	6343	3	US-08-581-148C-30
2	209.2	25.4	6550	3	US-09-037-319A-1
3	209.2	25.4	6550	3	US-09-037-319A-1
4	209.2	25.4	9299	3	US-09-037-319A-15
5	209.2	25.4	9299	3	US-09-037-319A-15
6	209.2	25.4	9408	3	US-09-037-319A-16
7	209.2	25.4	9408	3	US-09-037-319A-16
8	110.2	13.4	720	3	US-09-950-933A-8
9	41.6	5.1	601	3	US-09-949-016-160080
10	41.6	5.1	43562	3	US-09-949-016-16222
11	38.4	4.7	68580	3	US-09-949-016-15844
12	37.4	4.5	105413	3	US-10-427-923-3
13	37.4	4.5	112219	3	US-09-949-016-12453
14	37.4	4.5	112222	3	US-09-949-016-14324
15	37.4	4.5	113186	3	US-09-949-016-17572
16	36.6	4.4	1141	3	US-09-806-708B-22
17	35.4	4.3	132456	3	US-09-949-016-13750
18	34.8	4.2	630	3	US-09-830-230A-56
19	34.8	4.2	630	3	US-09-830-230A-55
20	34.2	4.2	601	3	US-09-949-016-81743
21	34.2	4.2	125192	3	US-09-949-016-14120
22	33.6	4.1	6434	3	US-09-949-016-1554
23	33.6	4.1	105168	3	US-09-949-016-13296
24	33.6	4.1	462589	3	US-09-949-016-12900

C 25	33.6	4.1	476044	3	US-09-949-016-12412	A
26	33.4	4.1	601	3	US-09-949-016-131416	A
27	33.4	4.1	601	3	US-09-949-002-3239	Ap
28	33.4	4.1	601	3	US-09-949-002-7323	Ap
C 29	33.4	4.1	26075	3	US-09-949-016-12004	A
C 30	33.4	4.1	26076	3	US-09-949-016-13041	A
31	33.4	4.1	105045	3	US-09-949-002-663	App
32	33.4	4.1	107045	3	US-09-949-002-772	App
33	33.4	4.1	124701	3	US-09-949-016-11817	A
34	33.4	4.1	124701	3	US-09-949-016-15439	A
35	33.4	4.1	187169	3	US-09-949-016-12776	A
36	33.4	4.1	191569	3	US-09-949-016-15940	A
37	33.2	4.0	57751	3	US-09-949-016-13631	A
C 38	33.2	4.0	106256	3	US-09-949-016-16558	A
C 39	33.2	4.0	163662	3	US-09-949-016-12545	A
C 40	33.2	4.0	163664	3	US-09-949-016-13546	A
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C 42	32.8	4.0	601	3	US-09-949-016-64741	A
43	32.8	4.0	601	3	US-09-949-016-90120	A
44	32.8	4.0	1141	3	US-09-806-708B-22	App1
C 45	32.6	4.0	601	3	US-09-949-016-108444	A

ALIGNMENTS

RESULT 1
US-08-581-148C-30
Sequence 30, Application US/08581148C
Patent No. 6060644
GENERAL INFORMATION:
APPLICANT: Schnable, Patrick S.
APPLICANT: Robertson, Donald S.
APPLICANT: Hansen, Joel D.
APPLICANT: Nikolau, Basil J.
APPLICANT: Xu, Xiaojie
APPLICANT: Xia, Yiji
TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,148C
FILING DATE: 29-DEC-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Larcher, Carol
REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 71380
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 6343 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORGANISM: Zea mays
INDIVIDUAL ISOLATE: Z.mays Glossy2 locus DNA

STATE: Indiana
COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,971
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6550 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: exon
LOCATION: 4201..4425
OTHER INFORMATION: /product= "Peroxidase"
FEATURE:
NAME/KEY: intron
LOCATION: 4426..5058
FEATURE:
NAME/KEY: exon
LOCATION: 5059..5250
FEATURE:
NAME/KEY: intron
LOCATION: 5251..5382
FEATURE:
NAME/KEY: exon
LOCATION: 5383..5548
FEATURE:
NAME/KEY: intron
LOCATION: 5549..5649
FEATURE:
NAME/KEY: exon
LOCATION: 5650..6065
FEATURE:
NAME/KEY: CDS
LOCATION: join(4201..4425, 5059..5250, 5383..5547, 5649
..6068)
US-09-643-971-1

Query Match 25.4%; Score 209.2; DB 3; Length 6550;
Best Local Similarity 90.1%; Pred. No. 3.4e-59;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;
QY 2 TGCACGGTACTCCAGTATAGACACAGCTAAACACACATAATG---CAGTGGTCATG 58
DB 1355 TGCACAGTACTCCAGTATAGACACACACATAATGATAATATACAGTGGTTATA 1414
QY 59 TCTAAACATGTGCTTACCATTATTCATTGTATCAATCAGAACATTCAATAAATTAAAGT 118
DB 1415 TCTAAACATGTGCTTACCATTATTCATTGTATCAATCAGAACATTCAATAAATTAAAGT 1474
QY 119 GACCAATCAGATAGTCTCTGTCGCCGAATATAGAGTAAAGACACTGTGCTTCGTCAAGA 178
DB 1475 GACCAATCAGTACGCTCTGCTCGAACATAGAGTAAAGACACTGTGCTTCGTCAAGA 1534
QY 179 TACATGCTTGAATTTTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAG 238
DB 1535 TACATGCTTGAATTTTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAG 1594
QY 239 ACACCCATTGTACATGCCCTAA 260

DB 1595 ACACCCATTGTACATGCTCTTA 1616
RESULT 4
US-09-097-319A-15
Sequence 15, Application US/09097319A
Patent No. 6384207
GENERAL INFORMATION:
APPLICANT: Ainley, Michael
APPLICANT: Armstrong, Katherine
APPLICANT: Belmar, Scott
APPLICANT: Folkerts, Otto
APPLICANT: Hopkins, Nicole
APPLICANT: Menke, Michael A.
APPLICANT: Paredy, Dayakar
APPLICANT: Petolino, Joseph F.
APPLICANT: Smith, Kelley
APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dowelanco Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,319A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 9299 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-09-097-319A-15

Query Match 25.4%; Score 209.2; DB 3; Length 9299;
Best Local Similarity 90.1%; Pred. No. 4.2e-59;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;
QY 2 TGCACGGTACTCCAGTATAGACACAGCTAAACACACATAATG---CAGTGGTCATG 58
DB 1402 TGCACAGTACTCCAGTATAGACACACATAATGATAATATACAGTGGTTATA 1461
QY 59 TCTAAACATGTGCTTACCATTATTCATTGTATCAATCAGAACATTCAATAAATTAAAGT 118
DB 1462 TCTAAACATGTGCTTACCATTATTCATTGTATCAATCAGAACATTCAATAAATTAAAGT 1521
QY 119 GACCAATCAGATAGTCTCTGTCGCCGAATATAGAGTAAAGACACTGTGCTTCGTCAAGA 178
DB 1522 GACCAATCAGTACGCTCTGCTCGAACATAGAGTAAAGACACTGTGCTTCGTCAAGA 1581
QY 179 TACATGCTTGAATTTTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAG 238
DB 1582 TACATGCTTGAATTTTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAG 1641
QY 239 ACACCCATTGTACATGCCCTAA 260

Db 1642 ACACCCATTGTACATGCTCTTA 1663

RESULT 5
US-09-643-971-15
; Sequence 15, Application US/09643971
; Patent No. 6699984
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; APPLICANT: Armstrong, Katherine
; APPLICANT: Belmar, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Hopkins, Nicole
; APPLICANT: Menke, Michael A.
; APPLICANT: Paredy, Dayakar
; APPLICANT: Petolino, Joseph F.
; APPLICANT: Smith, Kelley
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dowelanco Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,971
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 4816
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9299 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
; US-09-643-971-15

Query Match 25.4%; Score 209.2; DB 3; Length 9299;
Best Local Similarity 90.1%; Pred. No. 4.2e-59;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;
QY 2 TGCACGGTACTCCAAAGTATTAAGACACAGCTAAACACAACTAATG---CAGTGGTCATG 58
Db 1402 TGCACAGTACTCCAAAGTATTAAGACACAACTAAACACAACTAATTAATACAGTGGTTATA 1461
QY 59 TCTAAACATGTGCTTACCATATTTCATTTGATCAATCAGAACATTCATTAATAATTAAGT 118
Db 1462 TCTAAACATGTGCTTACCATATTTCATTTGATCAATCAGAACATTCATTAATAATTAAGT 1521
QY 119 GACCAATCAGATAGTCTCTGTCGCGAATATAGAGCTAAGACACTGTGCTTCGTCAGA 178
Db 1522 GACCAATCAGTACGCTCTCTGTCGCGAATATAGAGCTAAGACACTGTGCTTCGTCAGA 1581
QY 179 TACATGCTTGAATTTTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTTTAC 238
Db 1582 TACATGCTTGAATTTTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTTTAC 1641
QY 239 ACACCCATTGTACATGCTCTTA 260
Db 1642 ACACCCATTGTACATGCTCTTA 1663

RESULT 6
US-09-097-319A-16
; Sequence 16, Application US/09097319A
; Patent No. 6384207
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; APPLICANT: Armstrong, Katherine
; APPLICANT: Belmar, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Hopkins, Nicole
; APPLICANT: Menke, Michael A.
; APPLICANT: Paredy, Dayakar
; APPLICANT: Petolino, Joseph F.
; APPLICANT: Smith, Kelley
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dowelanco Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,319A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 4816
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
; US-09-097-319A-16

Query Match 25.4%; Score 209.2; DB 3; Length 9408;
Best Local Similarity 90.1%; Pred. No. 4.3e-59;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;
QY 2 TGCACGGTACTCCAAAGTATTAAGACACAGCTAAACACAACTAATG---CAGTGGTCATG 58
Db 1408 TGCACAGTACTCCAAAGTATTAAGACACAACTAAACACAACTAATTAATACAGTGGTTATA 1467
QY 59 TCTAAACATGTGCTTACCATATTTCATTTGATCAATCAGAACATTCATTAATAATTAAGT 118
Db 1468 TCTAAACATGTGCTTACCATATTTCATTTGATCAATCAGAACATTCATTAATAATTAAGT 1527
QY 119 GACCAATCAGATAGTCTCTGTCGCGAATATAGAGCTAAGACACTGTGCTTCGTCAGA 178
Db 1528 GACCAATCAGTACGCTCTCTGTCGCGAATATAGAGCTAAGACACTGTGCTTCGTCAGA 1587
QY 179 TACATGCTTGAATTTTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTTTAC 238
Db 1588 TACATGCTTGAATTTTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTTTAC 1647
QY 239 ACACCCATTGTACATGCTCTTA 260
Db 1648 ACACCCATTGTACATGCTCTTA 1669

RESULT 7
US-09-643-971-16
; Sequence 16, Application US/09643971
; Patent No. 6699984
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; APPLICANT: Armstrong, Katherine
; APPLICANT: Belmar, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Hopkins, Nicole
; APPLICANT: Menke, Michael A.
; APPLICANT: Paredy, Dayakar
; APPLICANT: Petolino, Joseph F.
; APPLICANT: Smith, Kelley
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DowElanco Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,971
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 4816
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
US-09-643-971-16

Query Match 25.4%; Score 209.2; DB 3; Length 9408;
Best Local Similarity 90.1%; Pred. No. 4.3e-59;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;
QY 2 TGCACGGTACTCCAAAGTATTAAGACACAGCTAAACACAAACATAATG---CAGTGGTCATG 58
Db 1408 TGCACAGTACTCCAAAGTATTAAGACACAACTAAACACAAACATAATAATACAGTGGTTATA 1467
QY 59 TCTAAACATGTGCTTACCATATTCATTGATCAATCAGACACATTCATTAATTAATTAAGT 118
Db 1468 TCTAAACATGTGCTTACCATATTCATTGATCAATCAGACACATTCATTAATTAATTAAGT 1527
QY 119 GACCAATCAGATAGTCTCCTGTCCGGAATATAGAGCTAAGACACATGCTCTTCGTCAAGA 178
Db 1528 GACCAATCAGTACGCTCCTGTCTCGAACATAGAGCTAAGACATGCTCTTCGTCAAGA 1587
QY 179 TACATGCTTTGAGATTTTTTACATTCACCCCTTAGACACACTCTTAAGACACAACTTAAG 238
Db 1588 TACATGCTTTAAGTTTTTTTATATTTACTCCCAAGACACACTCTTAAGACACAACTTAAG 1647
QY 239 ACACCCATTGTACATGCGCTTAA 260
Db 1648 ACACCCATTGTACATGCTCTTA 1669

RESULT 8
US-09-950-933A-8
; Sequence 8, Application US/09950933A
; Patent No. 6875907
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro, Pedro
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/238472
; CURRENT APPLICATION NUMBER: US/09/950,933A
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (119)...(403)
US-09-950-933A-8

Query Match 13.4%; Score 110.2; DB 3; Length 720;
Best Local Similarity 90.1%; Pred. No. 2.2e-26;
Matches 118; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 CTGCACGGTACTCCAAAGTATTAAGACACAGCTAAACACAAACATAATGCGTGGTCATGTC 60
Db 578 CTGCACGGTACTCCAAAGTATTAAGACACAGCTAAACACAAACATAATGCGTGGTCATGTC 637
QY 61 TAAACATGTGCTTACCATATTCATTGTATCAATCAGACATTCATTAATTAATTAAGTGA 120
Db 638 TAAACATGTGCTTACCATATTCATTGTATCAATCAGACATTCATTAATTAATTAAGTGA 697
QY 121 CCAATCAGATA 131
Db 698 CCAAAAAAAAAA 708

RESULT 9
US-09-949-016-160080/c
; Sequence 160080, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160080
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-160080
Query Match 5.1%; Score 41.6; DB 3; Length 601;
Best Local Similarity 53.8%; Pred. No. 0.0027;
Matches 86; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 246 TTGTACATGCCCTTAAGTGGCAGCCGCTACGTAGGGGCTATTCAAGAACCAACCATGTGACAG 305

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Db 241 TTCTCAAGATTAATACTGGGACCAATATATGGCAGGCAATTTGAAGAACTTGCCTTGAGAGA 182
Qy 306 TTGTTGCAACGTGAATGTTATTTCTTCAGATTAAAGCTAAATTTAGACTGATGACAG 365
Db 181 TTGTGAATTCCTTATTATTAGAACGATTCAGATTAGATAAAGTCTTATTGACAGATGTTG 122
Qy 366 CTGCAATTCATAGACACAAAACACAGTGTAGAGCCGTATA 405
Db 121 ATGAGATTCTTTTCAGTGAAGAAGAGTAGAGAGGAGTTAAA 82

RESULT 10
US-09-949-016-16222/c
; Sequence 16222, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16222
; LENGTH: 43562
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(43562)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16222

Query Match 5.1%; Score 41.6; DB 3; Length 43562;
Best Local Similarity 53.8%; Pred. No. 0.039;
Matches 86; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 246 TTGTACATGCCCTACTGCGACCGCTAGTAGGGCTATTCAAGAACCAACCATGTACAG 305
Db 32557 TTCTCAAGATTAATACTGGGACCAATATATGGCAGGCAATTTGAAGAACTTGCCTTGAGAGA 32498
Qy 306 TTGTTGCAACGTGAATGTTATTTCTTCAGATTAAAGCTAAATTTAGACTGATGACAG 365
Db 32497 TTGTGAATTCCTTATTATTAGAACGATTCAGATTAGATAAAGTCTTATTGACAGATGTTG 32438
Qy 366 CTGCAATTCATAGACACAAAACACAGTGTAGAGCCGTATA 405
Db 32437 ATGAGATTCTTTTCAGTGAAGAAGAGTAGAGAGGAGTTAAA 32398

RESULT 11
US-09-949-016-15844
; Sequence 15844, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15844
; LENGTH: 68580
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15844

Query Match 4.7%; Score 38.4; DB 3; Length 68580;
Best Local Similarity 48.6%; Pred. No. 0.62;
Matches 105; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

Qy 376 TAGAGACAAAAACAGTGTAGAAGCCGTATTAAGCAATTAAGCAAAACAAAGCAACATTGCTTA 435
Db 19119 TAAAAAATAAACAACACAGAAACCTCTTAACCTTATGTTTACATGAACACACTGGCTG 19178
Qy 436 GCTACAACCAATTTGCTGGGCTTCCATGGGCATCGCAGAAAGTATTTGGCTGCATATTGC 495
Db 19179 TGCCATCATTTTACTGAAAAAGGTACCAAGGTCAATGATAAATAATATATAATATATTTTC 19238
Qy 496 TGAATTTATAGCGAGGCGCCCAAGCCCATCACTTCAGTTCGAGGTGAGCATTTGTACTTTT 555
Db 19239 TAAATACATTCCTTCTTACCAGGCACCTTAAAAACCTGTTGTAGCTTAACCTTCTAATGAT 19298
Qy 556 GTTAAACGCTCTCGATAAAATTTGTTTCACCTTAAAAATAGA 591
Db 19299 GTTAAATGACTTGATCAACATTTGCACCTTGATTAACA 19334

RESULT 12
US-10-427-923-3
; Sequence 3, Application US/10427923
; Patent No. 6916643
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001365
; CURRENT APPLICATION NUMBER: US/10/427,923
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 105413
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(105413)
; OTHER INFORMATION: n = A,T,C or G
US-10-427-923-3

Query Match 4.5%; Score 37.4; DB 3; Length 105413;
Best Local Similarity 49.2%; Pred. No. 1.8;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 4 CACGGTACTCCAAGTATTAAGACACAGCTAAACACACACATTAATGCAGTGGTCATGCTAA 63
Db 60593 CATAGTATATATATATATATATATATATATATATATATATATATATATATATATATAT 60652
Qy 64 AACATGTGCTTACCATATTCATTGTATCAATCAAGAACATCAATAAATAAAGTGACCA 123
Db 60653 CACATAGTATATATATATATATATATATATATATATATATATATATATATATATATAT 60712
Qy 124 ATCAGATAGTCTCCTGTGCCGAATATAGAGCTAGACACTGTGCTTCTGCTCAAGATACAT 183
Db 60713 ATCAGATAGTATATATATATATATATATATATATATATATATATATATATATATATAT 60772
Qy 184 GCTCTGAGATTTTTCAT 202
Db 60773 ATCAGATAGTATATATATATATATATATATATATATATATATATATATATATATATAT 60791
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RESULT 13

US-09-949-016-12453
; Sequence 12453, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF.
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12453
; LENGTH: 112219
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(112219)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12453

Query Match 4.5%; Score 37.4; DB 3; Length 112219;
Best Local Similarity 49.2%; Pred. No. 1.8;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
Qy 4 CACGGTACTCCAAGTATAAGACACAGCTAAACACACATAATGCGAGTGTCTAA 63
Db 60575 CATAGTATATAATATAATATATATATATATATATATATATATATATATAT 60634
Qy 64 AACATGTCTTACCATATTCATTCATCATCAGACATTCATTAATTAAGTGACCA 123
Db 60635 CACATAGTATATAATATATATATATATATATATATATATATATATATATAT 60694
Qy 124 ATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAGACACTGTCTTCGTCAGATACAT 183
Db 60695 ATCAGATAGTATATAATATATATATATATATATATATATATATATATATATAT 60754
Qy 184 GTCTTGAGATTTTTTACAT 202
Db 60755 ATCAGATAGTATATAATAT 60773

RESULT 14

US-09-949-016-14324
; Sequence 14324, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14324
; LENGTH: 112222

; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(112222)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14324
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Best Local Similarity 49.2%; Pred. No. 1.8;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
Qy 4 CACGGTACTCCAAGTATAAGACACAGCTAAACACACATAATGCGAGTGTCTAA 63
Db 60575 CATAGTATATAATATAATATATATATATATATATATATATATATATATATAT 60634
Qy 64 AACATGTCTTACCATATTCATTCATCATCAGACATTCATTAATTAAGTGACCA 123
Db 60635 CACATAGTATATAAT 60694
Qy 124 ATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAGACACTGTCTTCGTCAGATACAT 183
Db 60695 ATCAGATAGTATATAAT 60754
Qy 184 GTCTTGAGATTTTTTACAT 202
Db 60755 ATCAGATAGTATATAATAT 60773

RESULT 15

US-09-949-016-17572
; Sequence 17572, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17572
; LENGTH: 113186
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17572

Query Match 4.5%; Score 37.4; DB 3; Length 113186;
Best Local Similarity 49.2%; Pred. No. 1.8;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
Qy 4 CACGGTACTCCAAGTATAAGACACAGCTAAACACACATAATGCGAGTGTCTAA 63
Db 61562 CATAGTATATAATATAATATATATATATATATATATATATATATATATATATAT 61621
Qy 64 AACATGTCTTACCATATTCATTCATCATCAGACATTCATTAATTAAGTGACCA 123
Db 61622 CACATAGTATATAAT 61681
Qy 124 ATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAGACACTGTCTTCGTCAGATACAT 183
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Searched:    41078325 seqs, 23393541228 residues

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Post-processing: Minimum Match 0%

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- 10: gb_gsa2:*
- 11: gb_gsa3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES

```

COMMENT:
Other_GSSs: Z04G1451V
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
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/organism="Zea mays"
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genomic DNA library"

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Best Local Similarity 99.1%; Pred.No.1.7e-156;
Matches 567; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OV 252 ATGCCCTAACTGGCACCCTACGTAGGGCGCTATTCAAGAACCAACCATGTACAGTTGTTG 311

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Best Local Similarity 92.8%; Pred. No. 9e-65;
Matches 269; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 CTCACGGTACTCAAGTATAAGACACAGCTAAACACACATTAATCCAGTGGTCAATGC 60
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QY 61 TAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCATAATAAATTAAGTGA 120
DB 711 TAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCATAATAAATTAAGTGA 652

QY 121 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGTCTTCGTCAGAGATA 180
DB 651 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGTCTTCGTCAGAGATA 592

QY 181 CATGCTCTTGAGATTTTACCATATTCATTGTATCAATCAGAACATTCATAATAAATTAAGTGA 240
DB 591 CGTGTCTTGAGATTTTACCATATTCATTGTATCAATCAGAACATTCATAATAAATTAAGTGA 532

QY 241 ACCATTGTATACGCTCCCTAACTGACCGCTACGTAGGGCTATTCAAGA 290
DB 531 ACCATTGTATACGCTCCCTAACTGACCGCTACGTAGGGCTATTCAAGA 482

RESULT 4
LOCUS CC331420 679 bp DNA linear GSS 16-MAY-2003
DEFINITION OMBK41TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBLa0384G09,
genomic survey sequence.
ACCESSION CC331420
VERSION CC331420.1 GI:30800591
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS White, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nurnberg, A., Robbins, D. and Lakey, N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
FEATURES
source Location/Qualifiers
1..679
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/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

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Matches 255; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTCACGGTACTCAAGTATAAGACACAGCTAAACACACATTAATCCAGTGGTCAATGC 60
DB 118 CTCACGGTACTCAAGTATAAGACACAGCTAAACACACATTAATCAAGTGGTCAATGC 177

QY 61 TAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCATAATAAATTAAGTGA 120

DB 178 TAAACATGTGTCTTCCCATATTCATTGTATCAATCAGAACATTCATAATAAATTAAGTGA 237
QY 121 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGTCTTCGTCAGAGATA 180
DB 238 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGTCTTCGTCAGAGATA 297
QY 181 CATGCTCTTGAGATTTTACCATATTCATTGTATCAATCAGAACATTCATAATAAATTAAGTGA 240
DB 298 CATGCTCTTGAGATTTTACCATATTCATTGTATCAATCAGAACATTCATAATAAATTAAGTGA 357
QY 241 ACCATTGTATACGCTCCCTAA 260
DB 358 ACCATTGTATACGCTCCCTAA 377

RESULT 5
LOCUS CW009430 847 bp DNA linear GSS 23-SEP-2004
DEFINITION ZMMBLa0012C07.r_ZMMBLa_Zea_mays_genomic_clone_ZMMBLa0012C07.3,
genomic survey sequence.
ACCESSION CW009430
VERSION CW009430.1 GI:52592072
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
TITLE 1 (bases 1 to 847)
JOURNAL ZMMBL sequences
COMMENT Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
Place: 0012 row: C column: 07
Class: BAC ends.
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 30.6%; Score 251.8; DB 10; Length 847;
Best Local Similarity 93.9%; Pred. No. 2.1e-63;
Matches 262; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 CTCACGGTACTCAAGTATAAGACACAGCTAAACACACATTAATCCAGTGGTCAATGC 60
DB 47 CTCACGGTACTCAAGTATAAGACACAGCTAAACACACATTAATCAAGTGGTCAATGC 106

QY 61 TAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCATAATAAATTAAGTGA 120
DB 107 TAAACATGTGTCTTACCATATTCATTGTATCAATCAGAACATTCATAATAAATTAAGTGA 166

QY 121 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGTCTTCGTCAGAGATA 180
DB 167 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGTCTTCGTCAGAGATA 226

QY 181 CATGCTCTTGAGATTTTACCATATTCATTGTATCAATCAGAACATTCATAATAAATTAAGTGA 240
DB 227 CATGCTCTTGAGATTTTACCATATTCATTGTATCAATCAGAACATTCATAATAAATTAAGTGA 286

RESULT 7
CW007582

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 777)
Wing, R., Luo, M., Soderlund, C. and Haller, K.

TITLE
ZMBL sequences

COMMENT
Unpublished (2004)

CONTACT: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: rwing@genome.arizona.edu

Plate: 0007 row: D column: 24

Class: BAC ends.

Location/Qualifiers

1..777

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="B73"

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/clone="ZMBL0007D24"

/tissue type="immature ears"

/lab host="DH10B T1 phage resistant"

/clone lib="ZMBL0a"

/note="Vector: pGIBAC1; Site_1: SalI; Site_2: SalI"

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: methylation filtered.

Location/Qualifiers

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/organism="Zea mays"

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methylation filtered genomic DNA library"

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 777)

Wing, R., Luo, M., Soderlund, C. and Haller, K.

TITLE

ZMBL sequences

COMMENT

Unpublished (2004)

CONTACT: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: rwing@genome.arizona.edu

Plate: 0007 row: D column: 24

Class: BAC ends.

Location/Qualifiers

1..777

/organism="Zea mays"

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/lab host="DH10B T1 phage resistant"

/clone lib="ZMBL0a"

/note="Vector: pGIBAC1; Site_1: SalI; Site_2: SalI"

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: methylation filtered.

Location/Qualifiers

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/organism="Zea mays"

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/notes="Vector: pBSK-; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 777)

Wing, R., Luo, M., Soderlund, C. and Haller, K.

TITLE

ZMBL sequences

COMMENT

Unpublished (2004)

CONTACT: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA</

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FEATURES
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ORIGIN
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Best Local Similarity 96.6%; Pred. No. 9.3e-63;
Matches 255; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 CTGCACGGTACTCCAGTATAGACACAGCTAAACACACAACTATGAGTGGTTCATGTC 60
DB 380 CTGCACGGTACTCCAGTATAGACACAACTAAACACACAACTATGAGTGGTTCATGTC 321
QY 61 TAAACATGCTCTTACCATATTTTACATTTTATCAATCAGAACATTCATTAATTAAGTGA 120
DB 320 TAAACATGCTCTTACCATATTTTACATTTTATCAATCAGAACATTCATTAATTAAGTGA 261
QY 121 CCAATCAGATAGTCTCTGTCGCGAATATAGAGCTTAAGACACTGTCTTCTGTCAGATA 180
DB 320 TAAACATGCTCTTACCATATTTTACATTTTATCAATCAGAACATTCATTAATTAAGTGA 201
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DB 181 CATGCTCTGAGATTTTACATTTTATCAATTTACCCCTTAGACACTCTTAAGACACTTAAGAC 240
DB 200 CATGCTCTGAGATTTTACATTTTATCAATTTACCCCTTAGACACTCTTAAGACACTTAAGAC 141
QY 241 ACCATTGTACATGCCCTTAAGTGG 264
DB 140 ACCATTGTACATGCCCTTAAGTGG 117

RESULT 11
LOCUS CL984256 979 bp DNA linear GSS 23-SEP-2004
DEFINITION ZMBHd000000000 r. ZMBHd Zea mays genomic clone ZMBHd000000000 3',
genomic survey sequence.
ACCESSION CL984256
VERSION CL984256.1 GI:5252334
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 979)
AUTHORS Ma, J., SanMiguel, P., Liu, R., Haller, K., Soderlund, C. and
Bennetzen, J.
TITLE ZMBH sequences
JOURNAL Unpublished (2004)
COMMENT Contact: Jeff Bennetzen
Bennetzen Lab
The University of Georgia
Department of Genetics, C426a Life Sciences Building, Athens, GA
30602, USA
Tel: 706-542-3698
Fax: 706-583-0972
Email: maize@uga.edu
Plate: 0001 row: n column: 07
Class: BAC ends.
Location/Qualifiers
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FEATURES
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DB 260 CTGCACGGTACTCCAGTATAGACACAGCTAAACACACAACTATTAAGTGA 319
QY 61 TAAACATGCTCTTACCATATTTTACATTTTATCAATCAGAACATTCATTAATTAAGTGA 120
DB 320 TAAACATGCTCTTACCATATTTTACATTTTATCAATCAGAACATTCATTAATTAAGTGA 379
QY 121 CCAATCAGATAGTCTCTGTCGCGAATATAGAGCTTAAGACACTGTCTTCTGTCAGATA 180
DB 380 CCAATCAGATAGTCTCTGTCGCGAATATAGAGCTTAAGACACTGTCTTCTGTCAGATA 439
QY 181 CATGCTCTGAGATTTTACATTTTATCAATTTACCCCTTAGACACTCTTAAGACACTTAAGAC 240
DB 440 CGTCTCTGAGATTTTACATTTTATCAATTTACCCCTTAGACACTCTTAAGACACTTAAGAC 499
QY 241 ACCATTGTACATGCCCTTAAGTGG 265
DB 500 ACCATTGTACATGCCCTTAAGTGG 524

RESULT 12
LOCUS CZ362236 893 bp DNA linear GSS 29-MAR-2005
DEFINITION ZMBHd0140018 r. ZMBH Zea mays genomic clone ZMBHd0140018 3', genomic
survey sequence.
ACCESSION CZ362236
VERSION CZ362236.1 GI:61972180
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 893)
AUTHORS Bharti, A.K., Nelson, A.B., Young, S., Keizer, G., Zohovetz, V., Fu, K.,
and Messing, J.
TITLE Construction, Sequencing and Characterization of a Fosmid Library
of the B73 Maize Genome
JOURNAL Unpublished (2005)
COMMENT Contact: Bharti, A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Freelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: fosmid ends.
Location/Qualifiers
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ORIGIN
Query Match 30.2%; Score 248.8; DB 10; Length 893;
Matches 255; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 1 CTGCACGGTACTCCAGTATAGACACAGCTAAACACACAACTATTAAGTGA 60
DB 260 CTGCACGGTACTCCAGTATAGACACAGCTAAACACACAACTATTAAGTGA 319
QY 61 TAAACATGCTCTTACCATATTTTACATTTTATCAATCAGAACATTCATTAATTAAGTGA 120
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QY 121 CCAATCAGATAGTCTCTGTCGCGAATATAGAGCTTAAGACACTGTCTTCTGTCAGATA 180
DB 380 CCAATCAGATAGTCTCTGTCGCGAATATAGAGCTTAAGACACTGTCTTCTGTCAGATA 439
QY 181 CATGCTCTGAGATTTTACATTTTATCAATTTACCCCTTAGACACTCTTAAGACACTTAAGAC 240
DB 440 CGTCTCTGAGATTTTACATTTTATCAATTTACCCCTTAGACACTCTTAAGACACTTAAGAC 499
QY 241 ACCATTGTACATGCCCTTAAGTGG 265
DB 500 ACCATTGTACATGCCCTTAAGTGG 524
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Qy	181	CATGTCCTTGAGATTTTTTACATTCACCCCTCCTAGACACACTCTTAAGACACAACTTTAAGAC	240
Db	93	CATGTCCTTGAGATTTTTTACATTCACCCCTCCTAGACACACTCTTAAGACACAACTTTAAGAC	34
Qy	241	ACCCATTGTACATGCCCTTAA	260
Db	33	ACCCATGTACATGCCCTTA	14
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LOCUS	CC397968	717 bp	DNA
DEFINITION	PHU8D37TD ZM_0.6_1.0 KB		linear
	genomic survey sequence.		GSS 19-MAY-2000
ACCESSION	CC397968		
VERSION	CC397968.1		
	GI:30878058		

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SOURCE
  ORGANISM
    Zea mays
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
  1 (bases 1 to 717)
  Whitelaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T.,
  Reenick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
  Bennetzen,J.
  Maize Genomics Consortium
  Unpublished (2003)
  Other_GSSs: PUHDC37TB
  Contact: Cathy Whitelaw
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA
  Tel: 301-838-5843
  Fax: 301-838-0208
  Email: whitelaw@tigr.org
  Seq primer: TP
  Class: sheared ends.
  Location/Qualifiers
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FEATURES
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		Matches 253;	Conservative	0;	Mismatches 8;	Indels	0;	Gaps	0
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Qy	61	TAAACAATGTGCTTTACCATATTTTCATTGTATCAATCAGACATTTCAATTAATTAAAGTGA	120						
Db	422	TAAACAATGTGCTTTACCATATTTTCATTGTACCAATCAAAACATTTCAATAAATTAAAGTGA	481						
Qy	121	CCAATCAGATAGTCTCTCTGTCCCGAATATAGAGCTATAGACACTGTGCTTCGTCCAAGATA	180						
Db	482	CCAATCAGATAGTCTCTCTGTCTCGAATATAGAGCTATAGACACACTGTGCTTCGTCCAAGATA	541						
Qy	181	CATGCTCTTGAGATTTTTTTTATCATTTTACCCCCCTAGACACACTCTTAAGACACAACCTTAAGAC	240						

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: March 5, 2006, 09:29:49 ; Search time 620 Seconds
(without alignments)
8846.842 Million cell updates/sec
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Gapop 10.0 , Gapext 1.0
Searched: 4996997 seqs, 3332346308 residues
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Listing first 45 summaries

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3: Geneseqn2000s.*
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5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2002bs.*
8: Geneseqn2003s.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004s.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	823	100.0		823	6	AAS96569	Aas96569 Corn prom
2	564	68.5		1587	6	AAS96566	Aas96566 Corn prom
C 3	231	28.1		1578	13	ADX48086	Adx48086 Plant full
4	227	27.6		6343	3	AAS57891	Aas57891 Maize glo
5	220.2	26.8		1326	13	ADX60974	Adx60974 Plant full
6	209.2	25.4		6550	2	Aav63717	Aav63717 Maize per
7	209.2	25.4		9299	2	Aav63730	Aav63730 Vector pl
8	209.2	25.4		9408	2	Aav63731	Aav63731 Vector pl
C 9	179.4	21.8		485	13	ADX49209	Adx49209 Plant full
C 10	123.2	15.0		1088	13	ADT17641	Adt17641 Plant cdn
11	110.2	13.4		720	6	AAL37816	Aal37816 Corn KCP-
12	99.2	12.1		737	13	ADX53136	Adx53136 Plant full
13	74.6	9.1		769	3	AAC43750	Aac43750 Zea mays
14	62	7.5		821	13	ADX33652	Adx33652 Plant full
15	60	7.3		1696	13	ADX61698	Adx61698 Plant full
16	59	7.2		791	13	ADX30094	Adx30094 Plant full
17	59	7.2		795	13	ADX30071	Adx30071 Plant full
18	56.8	6.9		765	13	ADX31426	Adx31426 Plant full
19	53.6	6.5		1090	13	ADX50035	Adx50035 Plant full

ALIGNMENTS

RESULT 1
AAS96569
ID AAS96569 standard; DNA; 823 BP.
XX AAS96569;
AC AAS96569;
DT 26-FEB-2002 (first entry)
XX
DE Corn promoter sequence #12.
XX
KW Corn; male reproductive tissue; plant regulatory sequence; Zea mays;
KW promoter; transcription regulation; operably linked gene; monocot; dicot;
KW wheat anther; plant fertility; insect tolerance; pathogen tolerance;
KW herbicide tolerance; ds.
XX Zea mays.
XX WO200183790-A2.
XX PD 08-NOV-2001.
XX PF 30-APR-2001; 2001WO-US013739.
XX PR 01-MAY-2000; 2000US-0201255P.
XX (MONS) MONSANTO TECHNOLOGY LLC.
XX Conner TW, Dubois P, Malven M, Masucci JD;
XX WPI; 2002-055481/07.
XX Novel promoters isolated from corn for controlling gene expression in
PT male reproductive tissues, such as anthers, tassels, and to regulate
PT transcription of target genes including genes for insect or pathogen
XX tolerance.
XX Claim 1; Page 113-114; 121pp; English.
XX The present invention relates to the isolation of plant regulatory
CC sequences from the male reproductive tissues of corn (Zea mays). The
CC promoter sequences, fragments, regions or cis elements of the sequences,
CC are capable of regulating transcription of an operably linked DNA

C	20	53.6	6.5	1318	13	ADO83463	Ado83463 Plant ful
C	21	50.6	6.1	505	13	ADX33788	Adx33788 Plant ful
C	22	50.6	6.1	2074	13	ADX52602	Adx52602 Plant ful
C	23	49	6.0	781	13	ADX33856	Adx33856 Plant ful
C	24	47.6	5.8	1412	13	ADX46949	Adx46949 Plant ful
C	25	44.6	5.4	110000	12	ADQ97047_1	Continuation (2 of
C	26	44.2	5.4	1027	13	ADO83991	Ado83991 Plant ful
C	27	44.2	5.4	1512	13	ADX52319	Adx52319 Plant ful
C	28	44.2	5.4	1538	13	ADX48874	Adx48874 Plant ful
C	29	43.4	5.3	271	12	ADQ04600	Adq04600 Maize hom
C	30	43.4	5.3	377	13	ADX10043	Adx10043 Plant ful
C	31	43.4	5.3	891	13	ADX34170	Adx34170 Plant ful
C	32	43.4	5.3	1184	13	ADX35171	Adx35171 Plant ful
C	33	43.4	5.3	1272	13	ADO83107	Ado83107 Plant ful
C	34	43.4	5.3	1676	13	ADX62396	Adx62396 Plant ful
C	35	43.4	5.3	1696	12	ADM47884	Adm47884 Polynucle
C	36	43.4	5.3	1699	13	ADX60046	Adx60046 Plant ful
C	37	43.4	5.3	1707	13	ADX63325	Adx63325 Plant ful
C	38	43.4	5.3	1807	13	ADX62639	Adx62639 Plant ful
C	39	43.4	5.3	2000	8	ADA71938	Ada71938 Rice gene
C	40	43.4	5.3	2025	3	AAC51726	Aac51726 Zea mays
C	41	43.4	5.3	2109	13	ADX64747	Adx64747 Plant ful
C	42	42.2	5.1	527	13	ADX29247	Adx29247 Plant ful
C	43	41.8	5.1	264	12	ADQ04637	Adq04637 Maize hom
C	44	41.8	5.1	281	12	ADQ04636	Adq04636 Maize hom
C	45	41.8	5.1	398	13	ADX12232	Adx12232 Plant ful

Db	1112	TTCATAGAGACAAAAACAGTGTAGAGCCGTATAGCAATTAAGCAAAACAAGCGAACATTG	1171
Qy	432	CTTAGCTACAAACCAATTTCCTGGGCTTCATAGGGCATCGCAGAAAGTATTGTGGCTGCATA	491
Db	1172	CTTAGCTACAAACCAATTTCCTGGGCTTCATAGGGCATCGCAGAAAGTATTGTGGCTGCATA	1231
Qy	492	TTGCTGAAATTTATAGCAGAGGCCCAAGGCCCATCACTTCACTTCGAGGTGAGCAATTTGTAC	551
Db	1232	TTGCTGAAATTTATAGCAGAGGCCCAAGGCCCATCACTTCACTTCGAGGTGAGCAATTTGTAC	1291
Qy	552	TTTTTGTAAAGTCTCGATAAATTTGTTCACTTAAATAGACCAGTTCAATTCCTGGTTCTA	611
Db	1292	TTTTTGTAAAGTCTCGATAAATTTGTTCACTTAAATAGACCAGTTCAATTCCTGGTTCTA	1351
Qy	612	GTCAACATGCTCTGATCCACGGGGAGCGAGGACGAATGTGTGGCCCGCCGCGAGTGAG	671
Db	1352	GTCAACATGCTCTGATCCACGGGGAGCGAGGACGAATGTGTGGCCCGCCGCGAGTGAG	1411
Qy	672	GCCAAAGCGAGCCCGGTCTGTCGGTCCAAACACACCCCTCGTTTACTATATATACACAGA	731
Db	1412	GCCAAAGCGAGCCCGGTCTGTCGGTCCAAACACACCCCTCGTTTACTATATATACACAGA	1471
Qy	732	CGCACGATACCCATATCGTGGTGTGAAGCAACTGAAAAACAGCCGAGCGATCTCCTCTC	791
Db	1472	CGCACGATACCCATATCGTGGTGTGAAGCAACTGAAAAACAGCCGAGCGATCTCCTCTC	1531
Qy	792	CCTCTCCCTCTCCGATCCATTTCTCCAGGGGAG	823
Db	1532	CCTCTCCCTCTCCGATCCATTTCTCCAGGGGAG	1563

RESULT 3	
ADX48086/c	
ID	ADX48086 standard; cDNA; 1578 BP.
XX	
AC	ADX48086;
XX	
DT	21-APR-2005 (first entry)
XX	
DE	Plant full length insert polynucleotide seqid 22826.
XX	
KW	plant protectant; plant growth regulant; gene therapy; plant;
KW	recombinant DNA construct; physical array; plant breeding marker;
KW	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW	extreme osmotic condition; pathogen tolerance; pest tolerance;
KW	growth rate; cell cycle pathway; disease resistance;
KW	galactomannan production; lignin production; plant growth regulator;
KW	yield; plant growth; plant development; seed oil; protein yield;
KW	protein content; gene; ss.
XX	
OS	Unidentified.
XX	
PN	US2004034888-A1.
XX	
PD	19-FEB-2004.
XX	
PF	28-APR-2003; 2003US-00425114.
XX	
PR	05-MAY-1999; 99US-00304517.
XX	
PR	05-NOV-2001; 2001US-00985678.
XX	
PA	(LIUJ/) LIU J.
PA	(ZHOU/) ZHOU Y.
PA	(KOVA/) KOVALIC D K.
PA	(SCRE/) SCREEN S E.
PA	(TABAJ/) TABASKA J E.
PA	(CAOY/) CAO Y.
XX	
PI	Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX	
DR	WPI; 2004-180133/17.
XX	

PT	New recombinant DNA construct, useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for conferring increased resistance to plant disease, or for improving yield.
XX	
PS	Claim 1; SEQ ID NO 2826; 15pp; English.
XX	
CC	The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.segdata.uspto.gov/sequence.html?DocID:2004034888 . The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the invention.
CC	
XX	
SQ	Sequence 1578 BP; 380 A; 391 C; 429 G; 378 T; 0 U; 0 Other;
	Query Match 28.1%; Score 231; DB 13; Length 1578;
	Best Local Similarity 92.4%; Pred. NO. 1.5e-63;
	Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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DB	1054 TGCACGGTACTCCAAGTATAAGACACACCTTAAACACACACATAATACAGTGGACGGTCT 995
QY	62 AAAACATGTGCTTTACCATATTCATTGTATCAATCAATCAGAACATTCAATAAATTAAGTGAC 121
DB	994 AAAACATGTGCTTTACCATATTAATGTACCAATCAGAGCAATTCATAATAAATTAAGTGAC 935
QY	122 CAATCAGATAGTCTCTGTCGCCGATATAGAGCTAAGACACATGTCGTCTTCGTCACAGATAC 181
DB	934 CAATCAGCTAGTCTCATGTCCTGAACATAGAGCTAAGACACTGTGCTTCGTCACAGATAC 875
QY	182 ATGCTCTTGAGATTTTTTACATTCACCCCTCCTAGACACACTCTTAAGACACACACTTAAGACA 241
DB	874 ATATCTTGAGTTTTTTTACATTCACCCCTCCTAAGACACACTCGAGACATCACTCAAGACA 815
QY	242 CCCATTGTACATGCCCTAACTCG 264
DB	814 CCCACTGTACATGCCCTAATCG 792
RESULT 4	
AAA57891	
ID	AAA57891 standard; DNA; 6343 BP.
XX	
AC	AAA57891;
XX	
DT	10-OCT-2000 (first entry)
XX	
DE	Maize glossy2 (gl2) gene.
XX	
KW	Maize; glossy2; gl2; cuticle; cuticular lipid biosynthesis;
KW	lipid composition; lipid quantity; disease resistance; pest resistance;
KW	wind resistance; frost resistance; UV resistance; transgenic plant;
XX	antisease inhibition; ds.
XX	
XX	Zea mays.
XX	
XX	US6060644-A.
PN	
XX	
PD	09-MAY-2000.

XX 29-DEC-1995; 95US-00581148.
XX 24-MAR-1994; 94US-00218028.
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
XX Schnable PS, Nikolau BJ, Xu X, Xia Y, Robertson DS, Hansen JD;
XX WPI; 2000-349707/30.
XX
XX Transforming plants such as maize and canola, for producing new plant
XX varieties having disease and pest resistance involves introducing
XX cuticular lipid genes into the plant genome.
XX
XX Example 7; Col 115-122; 69pp; English.
XX
XX The invention relates to transforming a plant cell with either a nucleic
XX acid encoding a plant cuticular lipid biosynthetic protein, or an
XX antisense nucleic acid sequence targeted to a plant cuticular lipid
XX gene, and then generating a plant from the plant cell. The cuticular
XX lipid genes that may be used in the invention are given in AA57871-
XX A57884, and AA57891. The cuticle consists of a meshwork (cutin) of cross-
XX esterified polymerised hydroxy-fatty acids embedded in a complex mixture
XX of nonpolar lipids (the cuticular wax). The cuticle protects and
XX strengthens the plants, prevents evaporation of internal fluids and
XX filters UV radiation. Mutations in the cuticular lipid genes affects the
XX quantity and composition of cuticular lipids; in maize, 17 loci (the
XX glossy (gl) genes) have been identified as being involved in cuticular
XX lipid biosynthesis or control. The method is useful for introducing a
XX nucleic acid into a cell preferably of maize, soybean, rapeseed, canola,
XX cotton, safflower, peanut, palm or sunflower plant and generating a plant
XX from the plant cell. The transformed plants have improved environmental
XX resistance relating to wind, frost, UV or drought; fungal, bacterial or
XX viral disease resistance; pest resistance; and altered lipid content in
XX seeds. The present sequence represents the maize glossy2 (gl2) gene
XX
XX Sequence 6343 BP; 1493 A; 1667 C; 1607 G; 1564 T; 0 U; 12 Other;
XX
XX Query Match 27.6%; Score 227; DB 3; Length 6343;
XX Best Local Similarity 93.9%; Pred. No. 6.6e-62;
XX Matches 247; Conservative 0; Mismatches 15; Indels 1; Gaps 1;
XX
XX 1 CTGCACGGTACTCCAAAGTATTAAGACACAGCTTAAACACAAATATGAGTGGTGTCTGTC 60
XX 3615 CTGCACGGTACTCCAAAGTATTAAGACACAACTTAAACACAAATATTAAGTGGTGTCTGTC 3674
XX
XX 61 TAAACATGTTCTTACCATTTTACATGTTATCAATCAATCAAGACATTCATTAATTAAGTGA 120
XX 3675 TAAACATGTTCTTACCATTTTACATGTTATTAATGTTACCAATCAAGGCAATTAATTAAGTGA 3734
XX
XX 121 CCAATCAGATAGTCTCTGTCGCCAATATAGAGTAAAGACACTGTCTTCGTCAGAGATA 180
XX 3735 CCAATCAGATAGTCTCTGTCGCCAATATAGAGTAAAGACACTGTCTTCGTCAGAGATA 3794
XX
XX 181 CATGCTTTGAGATTTTACATTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
XX 3795 CATGCTTTGAGATTTTACATTTACATTTACCTCTAGACACACTCTTAAGACACAACTTAAGAC 3854
XX
XX 241 A-CCCATGTTACATGCCCTTAATCT 262
XX 3855 ACCCCACGGTACATGCCCTTAATCT 3877
XX
XX RESULT 5
XX ADX60974
XX ID ADX60974 standard; cDNA; 1326 BP.
XX AC ADX60974;
XX XX
XX 21-APR-2005 (first entry)
XX DE Plant full length insert polynucleotide seqid 31817.

XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactonnanan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
XX
XX Unidentified.
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XX US2004034888-A1.
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX 03-NOV-2001; 2001US-00985678.
XX
XX (LIU//) LIU J.
XX (ZHOU//) ZHOU Y.
XX (KOVA//) KOVALIC D K.
XX (SCRE//) SCREEN S E.
XX (TAB//) TABASKA J E.
XX (CAO//) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 31817; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX polynucleotide that can be used in the recombinant DNA construct of the
XX invention.
XX
XX Sequence 1326 BP; 353 A; 297 C; 299 G; 377 T; 0 U; 0 Other;
XX
XX Query Match 26.8%; Score 220.2; DB 13; Length 1326;
XX Best Local Similarity 91.1%; Pred. No. 4.4e-60;
XX Matches 245; Conservative 0; Mismatches 23; Indels 1; Gaps 1;
XX
XX 1 CTGCACGGTACTCCAAAGTATTAAGACACAGCTTAAACACAAATATGAGTGGTGTCTGTC 60
XX 134 CTGCACGGTACTATAGTATTAAGACACAACTTAAACACAAATATGAGTGGTGTCTGTC 193
XX
XX 61 TAAACATGTTCTTACCATTTTACATGTTATCAATCAATCAATTAATTAAGTGA 120
XX 194 TAAACATGTTCTTACCATTTTACATGTTATCAATCAATCAATTAATTAAGTGA 253
XX
XX 121 CCAATCAGATAGTCTCTGTCGCCAATATAGAGTAAAGACACTGTCTTCGTCAGAGATA 180

Db 254 CCTATCAGCTAGTCTCTGCTCCAAACATAGACATGCTGCTCAGATA 313
Oy 181 CATGCTTGACATTTTACATTCACCCCTAGACACACCTCTTAAGACAACTTAAGAC 240
Db 314 CATGCTTGAGTTTTTTTACATTTCA-CCCTTTAGACACACTTTAAGACACAACTTAAGAC 372
Oy 241 ACCCATTTGATCATGCTCCCTAACTGGCAGCG 269
Db 373 ACATATTGATCATGCTCCCTAAGGGAGATCG 401

RESULT 6
AAV63717
ID AAV63717 standard; DNA; 6550 BP.
XX AAV63717;
XX
XX 12-APR-1999 (first entry)
XX
DE Maize per5 root preferential cationic peroxidase gene.
XX
KW Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root; ds.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT promoter 1..4215
FT /tag= a
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 1..4200
FT /tag= c
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 1..4148
FT /tag= b
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 2532..4215
FT /tag= f
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 2532..4200
FT /tag= e
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 2532..4148
FT /tag= d
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 3187..4215
FT /tag= i
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 3187..4200
FT /tag= h
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 3187..4148
FT /tag= g
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 4086..4215
FT /tag= l
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 4086..4200
FT /tag= k
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 4086..4148
FT /tag= j
FT /note= "this region is specifically claimed in Claim 1"
FT CDS 4201..6068
FT /tag= m
FT /product= "peroxidase"
FT /note= "contains introns"
FT exon 4201..4425
FT /tag= n
FT /note= "contains introns"
FT misc_feature 4420..5064
FT /tag= o
FT /note= "this sequence is specifically claimed in Claim 2"

FT intron 4426..5058
FT /tag= p
FT /number= 1
FT /note= "this intron is specifically claimed in Claim 2"
FT exon 5059..5250
FT /tag= q
FT /number= 2
FT misc_feature 5245..5388
FT /tag= r
FT /note= "this sequence is specifically claimed in Claim 2"
FT intron 5251..5382
FT /tag= s
FT /number= 2
FT /note= "this intron is specifically claimed in Claim 2"
FT exon 5383..5548
FT /tag= t
FT misc_feature 5542..5654
FT /tag= u
FT /note= "this sequence is specifically claimed in Claim 2"
FT misc_feature 5542..5654
FT /tag= x
FT /note= "this sequence is specifically claimed in Claim 2"
FT intron 5549..5649
FT /tag= v
FT /number= 3
FT /note= "this intron is specifically claimed in Claim 2"
FT exon 5650..6065
FT /tag= w
FT /number= 4
FT 3'UTR 6068..6431
FT /tag= y
FT /note= "transcription termination sequence, specifically claimed in Claim 3"
FT
FT
XX WO9856921-A1.
XX
XX 17-DEC-1998.
XX
XX 10-JUN-1998; 98WO-US011921.
XX
XX 12-JUN-1997; 97US-0049752P.
XX
XX (DOWC) DOW AGROSCIENCES-LLC.
XX
XX Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA,
XX Paredy D, Petolino JP, Smith K, Woosley A;
XX WPI; 1999-080904/07.
XX P-PSDB; AAW87893.
XX
XX New isolated regulatory sequences for transgenic plants - which are
XX derived from the maize root preferential cationic peroxidase protein
XX (per5) gene.
XX
XX Claim 1; Page 84-89; 150pp; English.
XX
XX This is the nucleotide sequence of the maize per5 root preferential
XX cationic peroxidase gene, which encodes a 333-amino acid peroxidase
XX polypeptide (see AAW87893). Genomic clones comprising per5 sequences were
XX isolated from a maize W22 genomic library using a probe based on isolated
XX per5 cDNA. Overlapping subfragments of the gene were sequenced to
XX determine the complete 550 bp sequence of the per5 gene. Regulatory
XX sequences derived from the per5 gene, including the promoter, introns and
XX 3' untranslated region (3'UTR), are used in claimed recombinant gene
XX cassettes for controlling expression of recombinant genes in selected
XX tissue, especially the root, of transformed plants, particularly maize.
XX The gene cassettes can be used for expression of heterologous genes such
XX as those that confer tolerance to herbicides, insects or viruses, and
XX genes that provide improved nutritional value or processing
XX characteristics to the plant. Use of the per5 3'UTR sequences provides
XX enhanced expression compared to similar gene cassettes utilising the nos
XX 3'UTR

```
XX SQ Sequence 6550 BP; 1844 A; 1427 C; 1346 G; 1933 T; 0 U; 0 Other;
Query Match 25.4%; Score 209.2; DB 2; Length 6550;
Best Local Similarity 90.1%; Pred. No. 4e-56;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;

Qy 2 TGCACGGTACTCCAGTATAGACACAGCTAAACACACACATATG---CAGTGGTCATG 58
Db 1355 TGCACAGTACTCCAGTATAGACACACACTAAACACACACATATATACAGTGGTTATA 1414

Qy 59 TCTAAACATGCTGCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAATTAAGT 118
Db 1415 TCTAAACATGCTGCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAATTAAGT 1474

Qy 119 GACCAATCAGATAGTCTCTCTCCGAATATAGAGCTAAGACACATGCTGCTTCGTCAAGA 178
Db 1475 GACCAATCAGCTAGCTCTCTCTCGAACATAGAGCTAAGACATGCTGCTTCGTCAAGA 1534

Qy 179 TACATGCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACACTTAAG 238
Db 1535 TACATGCTTGAAGTTTTTATATTCATCTCCCAAGACACACTCTAAGACACACTTAAG 1594

Qy 239 ACACCATGTTACATGCGCCTAA 260
Db 1595 ACACCATGTTACATGCTCTTA 1616

RESULT 7
AAV63730
ID AAV63730 standard; DNA; 9299 BP.
XX AC AAV63730;
XX
XX 12-APR-1999 (first entry)
XX DE Vector plasmid PerGUS16.
XX Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root;
KW vector; plasmid PerGUS16; beta-glucuronidase; uidA; reporter gene; ds;
KW circular; cyclic.
XX
XX Escherichia coli.
XX
XX Zea mays.
XX OS Agrobacterium tumefaciens.
XX OS Synthetic.
XX OS Chimeric.
XX
XX Key Location/Qualifiers
FT Promoter 48..4247
FT /tag= a
FT /note= "per5 promoter and untranslated leader"
FT exon 4248..4263
FT /tag= b
FT /note= "per5 exon 1"
FT CDS 4264..6068
FT /tag= c
FT /product= "beta-glucuronidase"
FT /note= "Escherichia coli uidA reporter gene"
FT 3'UTR 6069..6111
FT /tag= d
FT /note= "3' untranslated region from pBI221"
FT 3'UTR 6122..6396
FT /tag= e
FT /note= "nos 3'UTR"
FT misc_feature 6397..6407
FT /tag= f
FT /note= "linker"
FT 6408..9299
FT misc_feature
FT /tag= g
FT /note= "Bluescript II SK-"
XX
XX W09856921-A1.
```

```
XX 17-DEC-1998.
XX PD
XX PF 10-JUN-1998; 98WO-US011921.
XX PR 12-JUN-1997; 97US-0049752P.
XX PA (DOWC) DOW AGROSCIENCES LLC.
XX PI Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA,
PI Pareddy D, Pecolino JF, Smith K, Woosley A;
XX WPI; 1999-080904/07.
XX
XX New isolated regulatory sequences for transgenic plants - which are
XX derived from the maize root preferential cationic peroxidase protein
XX (per5) gene.
XX
XX Example 11; Page 108-112; 150pp; English.
XX
XX This is the nucleotide sequence of PerGUS, a plasmid containing 4 kb of
XX the maize root preferential cationic peroxidase per5 gene comprising the
XX per5 promoter, untranslated leader, and the first 5 codons of the coding
XX region (i.e., nucleotides 1-4200 of the sequence given in AAV63717), as
XX well as the GUS gene, and the nos 3' untranslated region (3'UTR). It does
XX not include an intron in the untranslated region. The invention relates
XX to new isolated regulatory sequences, especially promoter, intron and
XX 3'UTR sequences, of the maize per5 gene. Claimed recombinant gene
XX cassettes comprising per5 regulatory sequences are used to control
XX expression of recombinant genes in selected tissue, especially the root,
XX of transformed plants, particularly maize
XX
XX SQ Sequence 9299 BP; 2573 A; 2114 C; 2158 G; 2453 T; 0 U; 1 Other;
Query Match 25.4%; Score 209.2; DB 2; Length 9299;
Best Local Similarity 90.1%; Pred. No. 4.8e-56;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;

Qy 2 TGCACGGTACTCCAGTATAGACACAGCTAAACACACACATATG---CAGTGGTCATG 58
Db 1402 TGCACAGTACTCCAGTATAGACACACACTAAACACACACATATATACAGTGGTTATA 1461

Qy 59 TCTAAACATGCTGCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAATTAAGT 118
Db 1462 TCTAAACATGCTGCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAATTAAGT 1521

Qy 119 GACCAATCAGATAGTCTCTCTCCGAATATAGAGCTAAGACACACTGCTTCGTCAAGA 178
Db 1522 GACCAATCAGCTAGCTCTCTCTCGAACATAGAGCTAAGACATGCTGCTTCGTCAAGA 1581

Qy 179 TACATGCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACACTTAAG 238
Db 1582 TACATGCTTGAAGTTTTTATATTCATCTCCCAAGACACACTCTAAGACACACTTAAG 1641

Qy 239 ACACCATGTTACATGCGCCTAA 260
Db 1642 ACACCATGTTACATGCTCTTA 1663

RESULT 8
AAV63731
ID AAV63731 standard; DNA; 9408 BP.
XX AC AAV63731;
XX
XX 12-APR-1999 (first entry)
XX DE Vector plasmid PERGUSPER3.
XX Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root;
KW vector; plasmid PERGUSPER3; beta-glucuronidase; uidA; reporter gene; ds;
KW circular; cyclic.
XX
```

OS Escherichia coli.
OS Zea mays.
OS Agrobacterium tumefaciens.
OS Synthetic.
OS Chimeric.
XX

Key Location/Qualifiers
FH misc_feature 1..42
FT /tag= a
FT /note= "polylinker site"
FT misc_feature 43..53
FT /tag= b
FT /note= "synthetic linker"
FT promoter 54..4253
FT /tag= c
FT /note= "per5 promoter and untranslated leader"
FT exon 4254..4269
FT /tag= d
FT /note= "per5 exon 1"
FT CDS 4266..6074
FT /tag= e
FT /product= "beta-glucuronidase"
FT /note= "Escherichia coli uidA reporter gene"
FT 3'UTR 6075..7117
FT /tag= f
FT 3'UTR 6140..6510
FT /tag= g
FT /note= "per5 3'UTR"
FT misc_feature 6517..8408
FT /tag= h
FT /note= "Bluescript II SK-"
XX

W09856921-A1.
XX
XX 17-DEC-1998.
XX
XX 10-JUN-1998; 98WO-US011921.
XX
XX 12-JUN-1997; 97US-0049752P.
XX
XX (DOWC) DOW AGROSCIENCES LLC.
XX
XX Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA;
XX Paredy D, Petolino JF, Smith K, Woosley A;
XX WPI; 1998-080904/07.
XX
XX New isolated regulatory sequences for transgenic plants - which are
XX derived from the maize root preferential cationic peroxidase protein
XX (per5) gene.
XX
XX Example 12; Page 113-117; 150pp; English.
XX
XX This is the nucleotide sequence of PERGUSPER3, a plasmid containing 4.2
XX kb of the maize root preferential cationic peroxidase per5 gene
XX comprising the per5 promoter, untranslated leader, and the first 5 codons
XX of the coding region (i.e. nucleotides 1-4200 of the sequence given in
XX AAV63717), as well as the GUS gene, and the per5 3' untranslated region
XX (3'UTR, i.e. nucleotides 6069-6439 of the sequence given in AAV63717). It
XX does not include an intron in the untranslated region. Experiments
XX demonstrated that the per5 promoter, in the absence of an intron, drives
XX constitutive expression of transgenes in rice. The invention relates to
XX new isolated regulatory sequences, especially promoter, intron and 3'UTR.
XX sequences, of the maize per5 gene. Claimed recombinant gene cassettes
XX comprising per5 regulatory sequences are used to control expression of
XX recombinant genes in selected tissue, especially the root, of transformed
XX plants, particularly maize
XX

Query Match 25.4%; Score 209.2; DB 2; Length 9408;
Best Local Similarity 90.1%; Pred. No. 4.9e-56;
SQ Sequence 9408 BP; 2591 A; 2138 C; 2178 G; 2500 T; 0 U; 1 Other;

Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;
Qy 2 TGCAGCGTACTCCAGTATTAAGACACAGCTTAAGACACAAATATG---CAGTGGTCATG 58
Db 1408 TGCACAGTACTCCAGTATTAAGACACAACTAAACACAAATAATAATACAGTGGTTATA 1467
Qy 59 TCTAAAAACATGTGTCTTACCATATTTCATTGTATCAATCAGAACATTCATTAATAAATTAAGT 118
Db 1468 TCTAAAAACATGTGTCTTACCATATTTCATTGTATCAATCAGAACATTCATTAATAAATTAAGT 1527
Qy 119 GACCAATCAGATAGTCTCTGTCCCGAATATAGAGCTAAGACACATGTGTCTTCTGTCGAAGA 178
Db 1528 GACCAATCAGTACGCTCTGTCTCGAAACATAGAGCTAAGACATGTGTCTTCTGTCGAAGA 1587
Qy 179 TACATGCTCTGAGATTTTATACATTCACCCCTAGACACACTCTAGACACACACTTAAG 238
Db 1588 TACATGCTCTGAGATTTTATACATTCACCCCTAGACACACTCTAGACACACACTTAAG 238
Qy 239 ACACCCATTGTACATGCCCTAA 260
Db 1648 ACACCCATTGTACATGCCCTTA 1669

*RESULT 9
ADX49209/c
ID ADX49209 standard; cDNA; 485 BP.
XX AC ADX49209;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polynucleotide seqid 23949.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
XX
XX Unidentified.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIUJ/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABA/) TABASKA J E.
XX (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 23949; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence.

CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID=2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

XX Sequence 485 BP; 120 A; 126 C; 129 G; 110 T; 0 U; 0 Other;

Query Match 21.8%; Score 179.4; DB 13; Length 485;
Best Local Similarity 94.4%; Pred. No. 4.3e-47;
Matches 186; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 64 AACATGTCCTTACCATATTCATTGTATCAATCAGACATTCATATAATTAAGTGACCA 123
DB 481 AAAACATGTCCTTATTCATTGTATCAATCAGACATTCATATAATTAAGTGACCA 422
QY 124 ATCAGATAGTCCTTGTCCGAAATATAGAGCTAGACACTGTGCTTGTCAAGATACAT 183
DB 421 ATCAGATAGTCCTTGTCCGAAATATAGAGCTAGACACTGTGCTTGTCAAGATACAT 362
QY 184 GTCCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGACACC 243
DB 361 GTCCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGACACC 302
QY 244 CATTGTACATGCCCTAA 260
DB 301 CACTGTACATGCCCTTA 285

RESULT 10

ID ADT17641/c
ADT17641 standard; cDNA; 1088 BP.

AC ADT17641;

DT 13-JAN-2005 (first entry)

DE Plant cDNA, Seq ID 2967.

KW Plant; ss; gene; transgenic; cold tolerance; growth rate;
KW drought tolerance; disease resistance; galactomannan production;
KW plant growth regulator; heat tolerance; herbicide tolerance;
KW lignin production; extreme osmotic condition tolerance;
KW pathogens resistance; pest resistance; yield improvement; seed oil yield;
KW seed protein yield.

OS Viridiplantae.

PN US2004216190-A1.

PD 28-OCT-2004.

PF 18-DEC-2003; 2003US-00739930.

PR 28-APR-2003; 2003US-00424599.

PR 28-APR-2003; 2003US-00425115.

PA (KOVA/) KOVALIC D K.

PI Kovalic DK;

XX WPI; 2004-757369/74.

XX New recombinant DNA constructs useful in the field of biochemistry and
PT genetics and in particular for producing transgenic plants with improved
PT biological characteristics.

XX Claim 1; SEQ ID NO 2967; 14pp; English.

XX The invention relates a recombinant DNA construct comprising a
CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
CC Arabidopsis, wheat and rape but the specification does not indicate which
CC sequences is derived from which organism. Also included is a method of
CC producing a plant having an improved property, comprising transforming a
CC plant with a recombinant DNA construct comprising a promoter region
CC functional in a plant cell operably joined to a polynucleotide encoding a
CC polypeptide associated with the property, and growing the transformed
CC plant. The property is selected from improving plant cold tolerance, for
CC manipulating growth rate in plant cells by modification of the cell cycle
CC pathway, for improving plant drought tolerance, for providing increased
CC resistance to plant disease, for galactomannan production, for production
CC of plant growth regulators, for improving plant heat tolerance, for
CC improving plant tolerance to herbicides, for increasing the rate of
CC homologous recombination in plants, for lignin production, for improving
CC plant tolerance to extreme osmotic conditions, for improving plant
CC tolerance to pathogens or pests, for yield improvement by modification of
CC photosynthesis, for modifying seed oil yield and/or content, for
CC modifying seed protein yield and/or content, for yield improvement by
CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
CC and for yield improvement by providing improved plant growth and
CC development under at least one stress condition. The polynucleotide may
CC also encode a plant transcription factor. The methods and compositions of
CC the present invention are useful in the field of biochemistry and
CC genetics, in particular for producing transgenic plants with improved
CC biological characteristics such as increased yield, improved plant
CC flow, increasing plant tolerance to cold or heat, improving plant
CC tolerance to extreme osmotic and drought conditions, and improving plant
CC tolerance to plant pests or pathogens. They can also be used in physical
CC arrays of molecules, plant breeding markers, computer-based storage and
CC analysis systems. The present sequence is one of the 5544 plant cDNA
CC sequences of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from USPTO at
CC segdata.uspto.gov/sequence.html?DocID=20040216190.

XX Sequence 1088 BP; 265 A; 261 C; 260 G; 302 T; 0 U; 0 Other;

Query Match 15.0%; Score 123.2; DB 13; Length 1088;

Best Local Similarity 91.0%; Pred. No. 1.1e-28;

Matches 142; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 105 CAATAAATTAAGTGACCAATCAGATAGTCCTGTCCGAAATATAGAGCTAAGACACTG 164

DB 1088 CAATAAATTAAGTGACCAATCAGATAGTCCTGTCTCGAATGAGCTAAGATACTG 1029

QY 165 TGTCTTCTGTCGAAGATACATGCTTTGAGATTTTACATTCACCCCTAGACACTCTA 224

DB 1028 TGTCTTCTGTC-AGATACATGCTTTGAGTGTTCATTCACCCCTAAACACTCTA 970

QY 225 AGACACAACTTAAGACACCCCATTTGATACATGCGCTAA 260

DB 969 AATCACAACTTAAGACACTCTATTGTATACATCCCTTA 934

RESULT 11

AAL37816

ID AAL37816 standard; DNA; 720 BP.

XX AAL37816;

XX 05-AUG-2002 (first entry)

DE Corn KCP-like protein encoding DNA, SEQ ID NO 8.

xx Antimicrobial; transgenic; plant; potato snakin antimicrobial protein;
KW GAS4; GAS45; GAST1 homologue; lysine- and cysteine- rich peptide;
KW KCP-like polypeptide; modulating; disease resistance; gene; ds.
XX
OS Zea mays.
XX
XX WO200222821-A2.
XX
XX 21-MAR-2002.
XX
XX 13-SEP-2001; 2001WO-US028429.
XX
XX 13-SEP-2000; 2000US-0232569P.
PR 11-SEP-2001; 2001US-00950933.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Simmons CR, Navarro Acevedo PA;
PI
XX WPI; 2002-425842/45.
DR P-PSDB; AAO21285.
DR
XX New polynucleotide encoding lysine- and cysteine-rich peptides-like
PT polypeptide useful for modulating the polypeptide level in a plant cell,
PT enhancing disease resistance.
XX
XX Claim 1; Page 118-119; 163pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a
CC polypeptide which is related to potato snakin antimicrobial protein and
CC GAS4 or GAS45 or GAST1 homologues, which is referred to as lysine- and
CC cysteine- rich peptides (KCP)-like polypeptide, having a nucleotide
CC sequence from 36 sequences of defined base pairs, given in the
CC specification. A recombinant expression cassette comprising the isolated
CC polynucleotide of the invention is useful for modulating the level of
CC (KCP)-like polypeptides in a plant cell, where the level of (KCP)-like
CC polypeptides is increased, and disease resistance is enhanced. This
CC polynucleotide sequence represents the DNA encoding a KCP-like protein of
CC the invention
XX
XX Sequence 720 BP; 195 A; 215 C; 163 G; 147 T; 0 U; 0 Other;
Query Match 13.4%; Score 110.2; DB 6; Length 720;
Best Local Similarity 90.1%; Pred. No. 1.5e-24;
Matches 118; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 CTGCACGGTACTCCAGTATAGACACAGCTAAACACACACATATGCGTGTGTC 60
DB 578 CTGCACGGTACTCCAGTATAGACACAGCTAAACACACACATATGCGTGTGTC 637
QY 61 TAAACATGTGCTTACCATATTCATTGATCAATGACAAACATTCATTAATTAAGTGA 120
DB 638 TAAACATGTGCTTACCATATTCATTGATCAATGACAAACATTCATTAATTAAGTGA 697
QY 121 CCAATCAGATA 131
DB 698 CCAAAAAAAA 708
RESULT 12
ADX53136
ID ADX53136 standard; cDNA; 737 BP.
XX
AC ADX53136;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 27876.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

XX extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
XX
OS Unidentified.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
PR 03-NOV-2001; 2001US-00985678.
XX
XX (LIUJ/) LIU J.
XX (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 27876; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.seqdata.ustpo.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Sequence 737 BP; 182 A; 228 C; 174 G; 153 T; 0 U; 0 Other;
Query Match 12.1%; Score 99.2; DB 13; Length 737;
Best Local Similarity 92.1%; Pred. No. 5.6e-21;
Matches 116; Conservative 0; Mismatches 8; Indels 2; Gaps 1;
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DB 614 CTGCACGGTACTCCAGTATAGACACAGCTAAACACACACATATGCGTGTGTC 671
QY 61 TAAACATGTGCTTACCATATTCATTGATCAATGACAAACATTCATTAATTAAGTGA 120
DB 672 TAAACATGTGCTTACCATATTCATTGATCAATGACAAACATTCATTAATTAAGTGA 731
QY 121 CCAATC 126
DB 732 CCAATC 737

RESULT 13
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ID AAC43750 standard; DNA; 769 BP.
XX
AC AAC43750;
XX
DT 18-OCT-2000 (first entry)
XX
DE Zea mays DNA fragment SEQ ID NO: 40373.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic; pathway;
KW promoter; termination sequence; corn; ss.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
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PR 01-JUN-1999; 99US-0137222P.
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PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
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PR 27-JUL-1999; 99US-0145919P.
PR 27-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
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PR 10-AUG-1999; 99US-0148319P.
PR 11-AUG-1999; 99US-0148341P.
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PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 18-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.

Qy 822 AG 823
||
Db 61 AG 62

RESULT 15
ADX61698
ID ADX61698 standard; cDNA; 1696 BP.

XX
AC ADX61698;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 32541.

XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.

XX
OS Unidentified.
XX
XX US2004034888-A1.
PN
XX
PD 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
PF
XX 06-MAY-1999; 99US-00304517.
PR
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.

XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI
XX WPI; 2004-180133/17.
DR
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
PT
XX
PS Claim 1; SEQ ID NO 32541; 15pp; English.

XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX

SQ Sequence 1696 BP; 440 A; 429 C; 386 G; 441 T; 0 U; 0 Other;
Query Match 7.3%; Score 60; DB 13; Length 1696;
Best Local Similarity 78.3%; Pred.No. 4.6e-08;
Matches 72; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 317 TGAATGGTTATTGGCTTCAGATTAAAGCTAATTATTATTAGACTGATGCAGCTGCAATTCAT 376
Db 702 TAAAGTAGCTGTTGCGATTAAAGCCGACTGTTTGGACTGCTGCAGCTGTAATCTAT 761
Qy 377 AGAGACAAAACACAGTGTAGAACCGCTATAAGC 408
Db 762 AGAGACAAAACACATTGTAGAACACAGTAGAAGC 793

Search completed: March 5, 2006, 13:39:26
Job time : 622 secs

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 09:51:22 ; Search time 4261 Seconds
(without alignments)
10979.151 Million cell updates/sec

Title: US-10-660-208-90

Perfect score: 823

Sequence: 1 ctgcagggtactccaagtat.....cgatccattctccaggcag 823

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	823	100.0	823	6	AX299949 Sequence
2	564	68.5	1587	6	AX299946 Sequence
3	252	30.6	149882	14	AC155395 Zea mays
4	251.8	30.6	182004	14	AC155608 Zea mays
5	249.8	30.4	110000	15	Continuation (2 of
6	242.6	29.5	193326	14	AC155578 Zea mays
7	241.2	29.3	148120	14	AC155517 Zea mays
8	236	28.7	112468	14	AC149836 Zea mays
9	236	28.7	143793	14	AC149827 Zea mays
10	235.2	28.6	1257	15	AF348367 Zea mays
11	234.4	28.5	117844	14	AC155360 Zea mays
12	234.4	28.5	170318	14	AC155367 Zea mays
13	227	27.6	6343	15	ZMGLOSSY
14	226.4	27.5	134692	14	AC151050 Zea mays
15	223.2	27.1	198102	14	AC145389 Zea mays
16	220	26.7	133685	14	AC155399 Zea mays
17	218.4	26.5	175006	14	AC155579 Zea mays
18	215.2	26.1	164241	14	AC155575 Zea mays

c 19	213.6	26.0	189962	14	AC148165
c 20	209.4	25.4	63760	14	AC147518
c 21	209.2	25.4	6550	6	BD132692
c 22	209.2	25.4	6550	6	AR208995
c 23	209.2	25.4	6550	6	AR482064
c 24	209.2	25.4	9299	6	BD132705
c 25	209.2	25.4	9299	6	AR209008
c 26	209.2	25.4	9299	6	AR482077
c 27	209.2	25.4	9408	6	BD132706
c 28	209.2	25.4	9408	6	AR209009
c 29	209.2	25.4	9408	6	AR482078
c 30	208.4	25.3	116794	14	AC149633
c 31	205.8	25.0	187674	14	AC149640
c 32	202.4	24.6	169976	15	AY883559
c 33	194	23.6	181757	14	AC146713
c 34	193.4	23.5	160351	14	AC148152
c 35	186	22.6	147470	15	AC157776
c 36	173	21.0	119531	14	AC155407
c 37	164.6	20.0	69497	14	AC149816
c 38	143.6	17.4	165688	14	AC155607
c 39	141.6	17.2	132900	14	AC166637
c 40	110.2	13.4	720	6	AR649754
c 41	110.2	13.4	720	6	AX406847
c 42	84.2	10.2	166981	14	AC145225
c 43	83.2	10.1	174838	14	AC155493
c 44	67.4	8.2	181475	14	AC155391
c 45	62	7.5	154044	14	AC150186

ALIGNMENTS

RESULT 1
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LOCUS Sequence 90 from Patent WO0183790.
DEFINITION AX299949
ACCESSION AX299949
VERSION AX299949.1 GI:17129440
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1
AUTHORS Conner,T.W., Dubois,P., Malven,M. and Masucci,J.D.
TITLE Plant regulatory sequences for selective control of gene expression
JOURNAL Patent: WO 0183790-A 90 08-NOV-2001;
Monsanto Technology LLC (US)

FEATURES
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ORIGIN

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Best Local Similarity 100.0%; Fred. No. 6.6e-219;
Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 181 CATGCTTCGAGATTTTTTACATTACCCCTCCCTAGACACACTCTTAAGACACAACTTAAGAC 240

Center name: TIGR
Seq_lib_id: ZGGR
----- Project information
Web site: <http://www.tigr.org/tdb/tgi/maize/>
Contact: maize@tigr.org

* NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 2004: contig of 2004 bp in length
* 2005 2104: gap of unknown length
* 2105 15140: contig of 13036 bp in length
* 15141 15240: gap of unknown length
* 15241 16541: contig of 1301 bp in length
* 16542 16641: gap of unknown length
* 16642 21576: contig of 4935 bp in length
* 21577 21676: gap of unknown length
* 21677 24623: contig of 2947 bp in length
* 24624 24723: gap of unknown length
* 24724 28116: contig of 3393 bp in length
* 28117 29534: contig of 1318 bp in length
* 29535 29634: gap of unknown length
* 29635 32648: contig of 3014 bp in length
* 32649 32748: gap of unknown length
* 32749 40512: contig of 7764 bp in length
* 40513 40612: gap of unknown length
* 40613 43861: contig of 3249 bp in length
* 43862 43961: gap of unknown length
* 43962 48429: contig of 4468 bp in length
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* 48530 59229: contig of 10700 bp in length
* 59230 59329: gap of unknown length
* 59330 60889: contig of 1560 bp in length
* 60890 65147: gap of unknown length
* 65148 65247: contig of 4158 bp in length
* 65248 67581: contig of 2333 bp in length
* 67582 68776: gap of unknown length
* 68777 68876: contig of 1096 bp in length
* 68877 85493: contig of 16617 bp in length
* 85494 85593: gap of unknown length
* 85594 90518: contig of 4924 bp in length
* 90519 90618: gap of unknown length
* 90619 111500: contig of 20883 bp in length
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* 111601 112664: contig of 1064 bp in length
* 112665 112764: gap of unknown length
* 112765 122909: contig of 10145 bp in length
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* 123010 127130: contig of 4121 bp in length
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* 130720 130819: gap of unknown length
* 130820 140093: contig of 9274 bp in length
* 140094 140193: gap of unknown length
* 140194 162843: contig of 22650 bp in length
* 162844 162943: gap of unknown length
* 162944 167186: contig of 4243 bp in length
* 167187 167286: gap of unknown length
* 167287 169330: contig of 2644 bp in length
* 169331 170030: gap of unknown length
* 170031 175431: contig of 5401 bp in length
* 175432 175531: gap of unknown length
* 175532 177305: contig of 1774 bp in length
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		28117. .28216			
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		29535. .29634			
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		32649. .32748			
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	gap	/estimated length=unknown			

Query Match 30.6%; Score 251.8; DB 14; Length 182004;
Best Local Similarity 93.9%; Pred. No. 4.8e-59;

ORIGIN

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Matches 262; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 CTGCACGCTACTCCAGTATAGACACAGCTAAACACAAATATGAGTGGTCTATGTC 60
Db 47274 CTGCACGCTACTCCAGTATAGACACAGCTAAACACAAATATGAGTGGTCTATGTC 47333
QY 61 TAAACATGTGTCTTACCATTATTCATTCATCAATCAGAACATTCATCAATTAAGTGA 120
Db 47334 TAAACATGTGTCTTATCATATTCATTCATCAATCAGAACATTCATCAATTAAGTGA 47393
QY 121 CCAATCAGATAGTCTCTGTCGCGAATATAGAGCTAGACACTGTGTTCTCGTCAAGATA 180
Db 47394 CCAATCAGATAGTCTCTGTCGCGAATATAGAGCTAGACACTGTGTTCTCGTCAAGATA 47453
QY 181 CATGCTTGAGATTTTACATTCACCCCTAGACACTCTTAAGACACAACTTAAGAC 240
Db 47454 CGTGTCTTGAGATTTTACATTCACCCCTAGACACTCTTAAGACACAACTTAAGAC 47513
QY 241 ACCATTGTACATGCGCTTAACTGCGACCGCTACGTAGGG 279
Db 47514 ACCATTGTACATGCGCTTAACTGCGACCGCTACGTAGGG 47552

RESULT 5
AY664417 1/c
WPCOMMENT Sequence split into 4 fragments LOCUS AY664417 Accession AY664417
Fragment Name Begin End
AY664417_0 1 110000
AY664417_1 100001 210000
AY664417_2 200001 310000
AY664417_3 300001 366120
Continuation (2 of 4) of AY664417 from base 100001 (AY664417 Zea mays cultivar Mol17 locu

Query Match 30.4%; Score 249.8; DB 15; Length 110000;
Best Local Similarity 93.9%; Pred. No. 1.7e-58;
Matches 260; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
QY 1 CTGCACGCTACTCCAGTATAGACACAGCTAAACACAAATATGAGTGGTCTATGTC 60
Db 88631 CTGCACGCTACTCCAGTATAGACACAACTAAACACAAATATGAGTGGTCTATGTC 88572
QY 61 TAAACATGTGTCTTACCATTATTCATTCATCAATCAGAACATTCATCAATTAAGTGA 120
Db 88571 TAAACATGTGTCTTACCATTATTCATTCATCAATCAGAACATTCATCAATTAAGTGA 88512
QY 121 CCAATCAGATAGTCTCTGTCGCGAATATAGAGCTAGACACTGTGTTCTCGTCAAGATA 180
Db 88511 CCAATCAGATAGTCTCTGTCGCGAATATAGAGCTAGACACTGTGTTCTCGTCAAGATA 88452
QY 181 CATGCTTGAGATTTTACATTCACCCCTAGACACTCTTAAGACACAACTTAAGAC 240
Db 88451 CATGCTTGAGATTTTACATTCACCCCTAGACACTCTTAAGACACAACTTAAGAC 88392
QY 241 ACCATTGTACATGCGCTTAACTGCGACCGCTACGTAG 277
Db 88391 ACCATTGTACATGCGCTTAACTGCGACCGCTACGTAG 88355

RESULT 6
AC155578
LOCUS AC155578 193326 bp DNA linear HTG 25-JAN-2005
DEFINITION Zea mays strain B73 clone ZMMB00190D10, *** SEQUENCING IN PROGRESS
***, 34 unordered pieces.
ACCESSION AC155578
VERSION AC155578.2 GI:58082437
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 193326)
```

```
AUTHORS Chan, A.P., Perle, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Uterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlffing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J., and
Quackenbush, J.
TITLE Consortium for Maize Genomics - BAC skin sequencing and assembly
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 193326)
AUTHORS Chan, A.P., Perle, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Uterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlffing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J., and
Quackenbush, J.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
REFERENCE 9712 Medical Center Dr, Rockville, MD 20850
AUTHORS 3 (bases 1 to 193326)
Chan, A.P., Perle, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Uterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlffing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J., and
Quackenbush, J.
TITLE Direct Submission
JOURNAL Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR),
REFERENCE 9712 Medical Center Dr, Rockville, MD 20850
AUTHORS On Jan 25, 2005 this sequence version replaced gi:57863099.
COMMENT ----- Trace submission
Center name: TIGR
Seq lib id: ZGES
----- Project information
Web site: http://www.tigr.org/tdb/cgi/maize/
Contact: maize@tigr.org
```

* NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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* 1 2168: contig of 2168 bp in length
* 2 2268: gap of unknown length
* 3 2269: contig of 5678 bp in length
* 4 7947: gap of unknown length
* 5 8047: contig of 6485 bp in length
* 6 14531: contig of 8374 bp in length
* 7 14532: gap of unknown length
* 8 23005: contig of 8374 bp in length
* 9 23006: gap of unknown length
* 10 23105: contig of 8086 bp in length
* 11 31191: contig of 8086 bp in length
* 12 31291: gap of unknown length
* 13 31292: contig of 9184 bp in length
* 14 40575: gap of unknown length
* 15 40576: contig of 4765 bp in length
* 16 45340: gap of unknown length
* 17 45341: gap of unknown length
* 18 50239: contig of 4799 bp in length
* 19 50240: gap of unknown length
* 20 50340: gap of unknown length
* 21 55709: contig of 5369 bp in length
* 22 55809: gap of unknown length
* 23 66590: contig of 10782 bp in length
* 24 66591: gap of unknown length
* 25 74475: contig of 7785 bp in length
* 26 74476: gap of unknown length
* 27 84289: contig of 9714 bp in length
* 28 84290: gap of unknown length
* 29 84390: contig of 2297 bp in length
* 30 86687: gap of unknown length
* 31 86787: contig of 2607 bp in length
* 32 89394: gap of unknown length
* 33 89395: contig of 9902 bp in length
* 34 99396: gap of unknown length
* 35 99496: contig of 5295 bp in length
* 36 104791: contig of 5295 bp in length
* 37 104791: gap of unknown length
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gap	/estimated length=unknown	120859.120958
gap	/estimated length=unknown	125844.125943
gap	/estimated length=unknown	129477.129576
gap	/estimated length=unknown	-134150.134249
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gap	/estimated length=unknown	151366.151465
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gap	/estimated length=unknown	179686.179785

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•
•
•
•

RESULT 7
AC155517/C

AC155517/C	AC155517	B73 clone ZMMBc0062P3,	148120 bp	DNA linear	HTG 25-JAN-2005
LOCUS DEFINITION	***, 15 unordered pieces.				
ACCESSION	AC155517				
VERSION	AC155517.2	GI:58082377			
KEYWORDS	HTG; HTGS_PHASE1.				
SOURCE	Zea mays				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS

Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.

Consortium for Maize Genomics - BAC skim sequencing and assembly

TITLE
JOURNAL
REFERENCE
AUTHORS

Unpublished
2 (bases 1 to 148120)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.

TITLE
JOURNAL

Direct Submission
Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr, Rockville, MD 20850

REFERENCE
AUTHORS

3 (bases 1 to 148120)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.

TITLE
JOURNAL

Direct Submission
Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr, Rockville, MD 20850

COMMENT

On Jan 25, 2005 this sequence version replaced gi:57863038.

----- Trace submission

Center name: TIGR

Seq lib id: ZOBH

----- Project information

Web site: <http://www.tigr.org/tcb/tgi/maize/>

Contact: maize@tigr.org

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 7711: contig of 7711 bp in length
* 7712 7811: gap of unknown length
* 7812 38165: contig of 30354 bp in length
* 38166 38265: gap of unknown length
* 38266 40248: contig of 1983 bp in length
* 40249 40348: gap of unknown length
* 40349 55752: contig of 15404 bp in length
* 55753 55852: gap of unknown length
* 55853 61693: contig of 5841 bp in length
* 61694 79902: contig of 18109 bp in length
* 79903 80002: gap of unknown length
* 80003 82646: contig of 2644 bp in length
* 82647 82746: gap of unknown length
* 82747 98869: contig of 16123 bp in length
* 98870 98969: gap of unknown length
* 98970 102329: contig of 3360 bp in length
* 102330 102429: gap of unknown length
* 102430 105931: contig of 3502 bp in length
* 105932 106031: gap of unknown length
* 106032 124298: contig of 18267 bp in length
* 124299 124398: gap of unknown length
* 124399 125579: contig of 1181 bp in length
* 125580 125679: gap of unknown length
* 125680 130751: contig of 5072 bp in length
* 130752 130851: gap of unknown length
* 130852 144420: contig of 13569 bp in length
* 144421 144520: gap of unknown length
* 144521 148120: contig of 3600 bp in length.

FEATURES
source

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/db_xref="taxon:4577"
/clone="ZMMBc0062P13"
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38166..38265
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55753..55852
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125580..125679
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ORIGIN

Query Match 29.38; Score 241.2; DB 14; Length 148120;
Best Local Similarity 95.0%; Pred.No.4.e-56;
Matches 249; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy. 1 CTGCACGGTACTCAAGTATAAGACACAGCTAAACACACATTAATGAGTGA 60
Db 145976 CTGCACGGTACTCAAGTATAAGACACAGCTAAACACACATTAATGAGTGA 145977
Qy 61 TAAACATGCTCTTACCATTATTCATTAATCAATCAAGACATTAATTAAGTGA 120
Db 145916 TAAACATGCTCTTACCATTATTCATTAATCAATCAAGACATTAATTAAGTGA 145857
Qy 121 CCAATCAGATAGTCTCTGTCCTCCGATATAGAGCTAGACACTGTGCTTCGTCGAAGATA 180
Db 145956 CCAATCAGTAGCTCTCTGTCCTCGAATAGAGCTAGACACTGTGCTTCGTCGAAGATA 145797
Qy 181 CATGCTCTGAGATTTTTCATCAATTCACCCCTAGACACACTCTTAAGACACAACCTTAAGAC 240
Db 145796 CATGCTCTGAGTTTTCATCAATTCACCCCTAGACACACTCTTAAGACACAACCTTAAGAC 145737
Qy 241 ACCATTTGATGCTGCTTAAT 262
Db 145736 ACTCAATTTGATGCTGCTTAAT 145715

RESULT 8

AC149836
LOCUS AC149836 112468 bp DNA linear HTG 03-FEB-2005
DEFINITION Zea mays clone ZMMBc0496L17, *** SEQUENCING IN PROGRESS ***; 2
ordered pieces.
ACCESSION AC149836
VERSION AC149836.2 GI:57790161
KEYWORDS HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 112468)
Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K. and Messing,J.
Zea mays, clone ZMMBBc0496L17
Unpublished

2 (bases 1 to 112468)
Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K., Messing,J., Abouelleil,A., Allen,N., Anderson,M., Anderson,S., Archichi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgaltier,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Menues,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 112468)
Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K., Messing,J., Abouelleil,A., Allen,N., Anderson,M., Anderson,S., Archichi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukhgaltier,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrim,J., Menues,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (03-FEB-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 14, 2005 this sequence version replaced gi:49035067.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Broad Institute of MIT and Harvard
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@broad.mit.edu

Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA (<http://pgir.rutgers.edu>)
Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona,

Tucson, AZ 85721, USA (<http://www.genome.arizona.edu>)

----- Project Information
Center project name: L30352
Center clone name: 496_L_17

* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
* 1 62677: contig of 62677 bp in length
* 62678 62777: gap of unknown length
* 62778 112468: contig of 49691 bp in length.

FEATURES
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gap

ORIGIN
Query Match 28.7%; Score 236; DB 14; Length 112468;
Best Local Similarity 94.2%; Pred. No. 1.3e-54;
Matches 245; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 CTGCACGGTACTCCAGTATAGACACAGCTTAAGACACATATGCAGTGGTCATGTC 60
Db 2368 CTGCACGGTACTCCAGTATAGACACAGCTTAAGACACATATGCAGTGGTCATGTC 2427

Qy 61 TAAACATGTCCTTACCATATTCATTTGATCATCAATCAGAACATTCATTAATTAAGTGA 120
Db 2428 TAAACATGTCCTTACCATATTCATTTGATCATCAATCAGAACATTCATTAATTAAGTGA 2487

Qy 121 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAGACACTGTCTTCTGCTCAAGATA 180
Db 2488 CCAATCAGTACGCTCTTGTCTCGAATATAGAGCTAGACACTGTCTTCTGCTCAAGATA 2547

Qy 181 CATGCTTGTAGATTTTATACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
Db 2548 CATGCTTGTGGTTTTTTTATATTACCCCTAGACACACTCTTAAGACACAACTTAAGAC 2607

Qy 241 ACCCATGTATCATGCCCTAA 260
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RESULT 9
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LOCUS Zea mays clone ZMMBBc0051H21, *** SEQUENCING IN PROGRESS ***, 8
DEFINITION unordered pieces.
ACCESSION AC149827
VERSION AC149827.2 GI:57790148
KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 143793)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K. and Messing,J.
TITLE Zea mays, clone ZMMBBc0051H21
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 143793)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K.,

KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE AUTHORS
Dietrich, C.R., Cui, F., Packila, M.L., Li, J., Ashlock, D.A., Nikolau, B.J. and Schnable, P.S.
1 (bases 1 to 1257)
the gl8 gene and sequences flanking Mu target-site duplications exhibit nonrandom nucleotide composition throughout the genome
Genetics 160 (2), 697-716 (2002)
11861572

TITLE
JOURNAL
PUBMED
REFERENCE AUTHORS
Dietrich, C.R., Packila, M.L., Li, J., Ashlock, D.A., Nikolau, B.J. and Schnable, P.S.
2 (bases 1 to 1257)
Direct Submission
Submitted (12-FEB-2001) Zoology and Genetics, Iowa State University, B420 Agronomy Hall, Ames, IA 50011, USA
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/mol_type="genomic DNA"
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/db_xref="taxon:4577"
946. .>1257
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946. .>1257
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/translation="MAGTCAHFLEFRAQPAWALALAAVGLLVAVRAARFALWVYAF
LRPGKPLRRYGAWAVTGTGIGRAVAFRLAASGLGLVGRNQEKLAAYAAEIKR
RH"

FEATURES
source
mRNA
CDS

ORIGIN
Query Match 28.6%; Score 235.2; DB 15; Length 1257;
Best Local Similarity 93.2%; Pred. No. 1.9e-54;
Matches 246; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 1 CTGCACGGTACTCCAGTATAGACACAGCTAAACACACATATGAGTGGTTCATGTC 60
DB 425 CTGCACGGTACTCCAGTATAGACACAGCTAAACACACATATGAGTGGTTCATGTC 366
QY 61 TAAACATGTGCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAAATGA 120
DB 365 TAAACATGTGCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAAATGA 306
QY 121 CCAATCAGATAGTCTCTGTCGCGAATATAGAGCTAAGACACTGTGCTTCGTCAGATA 180
DB 305 CCAATCAGATAGTCTCTGTCGCGAATATAGAGCTAAGACACTGTGCTTCGTCAGATA 246
QY 181 CATGCTTCAGATTTTTCATTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 240
DB 245 CTGTCCTTCAGATTTTTCATTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 186
QY 241 ACCCATTTGATGCTGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 264
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RESULT 11
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LOCUS
DEFINITION Zea mays strain B73 clone ZNM5Bb0026K01, *** SEQUENCING IN PROGRESS
***, 17 unordered pieces.
ACCESSION AC155360
VERSION AC155360.2 GI:58082223
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 117844)
Chan, A.P., Perle, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Uterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.
Consortium for Maize Genomics - BAC skim sequencing and assembly
Unpublished
2 (bases 1 to 117844)
Chan, A.P., Perle, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Uterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.
Direct Submission
Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr, Rockville, MD 20850
3 (bases 1 to 117844)
Chan, A.P., Perle, G., Zheng, L., Cheung, F., Lee, D., Koo, H., Uterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M., Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T., Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and Quackenbush, J.
Direct Submission
Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr, Rockville, MD 20850
On Jan 25, 2005 this sequence version replaced gi:57862881.
----- Trace submission
Center name: TIGR
Seq_id: ZONE
----- Project information
Web site: http://www.tigr.org/tdb/cgi/maize/
Contact: maize@tigr.org

* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 12874: contig of 12874 bp in length
* 12875 12974: gap of unknown length
* 12975 15110: contig of 2136 bp in length
* 15111 15210: gap of unknown length
* 15211 31668: contig of 16458 bp in length
* 31669 31769: gap of unknown length
* 31769 39874: contig of 8105 bp in length
* 39874 48625: gap of unknown length
* 48625 48725: gap of unknown length
* 48725 55833: contig of 7108 bp in length
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* 55934 57365: contig of 1432 bp in length
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* 57465 59139: contig of 1674 bp in length
* 59139 59240: gap of unknown length
* 59240 67542: contig of 8303 bp in length
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* 67643 69850: contig of 2208 bp in length
* 69850 69951: gap of unknown length
* 69951 74443: contig of 4493 bp in length
* 74443 74544: gap of unknown length
* 74544 93153: contig of 18610 bp in length
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* 93254 98654: contig of 5401 bp in length
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* 102210 102310: gap of unknown length
* 102310 102311: gap of unknown length

* 28151 30686: contig of 2536 bp in length
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* 42197 80810: contig of 38614 bp in length
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* 114450 117461: contig of 3013 bp in length
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* 117562 119699: contig of 2138 bp in length
* 119700 119799: gap of unknown length
* 119800 122051: contig of 2252 bp in length
* 122052 122151: gap of unknown length
* 122152 124315: contig of 2164 bp in length
* 124316 124415: gap of unknown length
* 124416 127911: contig of 3496 bp in length
* 127912 128011: gap of unknown length
* 128012 129528: contig of 1517 bp in length
* 129529 129628: gap of unknown length
* 129629 132542: contig of 2914 bp in length
* 132543 132642: gap of unknown length
* 132643 134392: contig of 1750 bp in length
* 134393 134492: gap of unknown length
* 134493 137476: contig of 2984 bp in length
* 137477 137576: gap of unknown length
* 137577 138544: contig of 968 bp in length
* 138545 138644: gap of unknown length
* 138645 146242: contig of 7598 bp in length
* 146243 146342: gap of unknown length
* 146343 150461: contig of 4119 bp in length
* 150462 150561: gap of unknown length
* 150562 158664: contig of 8103 bp in length
* 158665 158764: gap of unknown length
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ORIGIN

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Matches 244; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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DB 99136 CTGACAGTACTCCAGGTATTAAGATACAACTAAACACAACTAATGCAGTGGTCATGTC 99195
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DB 99196 TAAACATGTGCTTACCATATTCATTTGTTATCAATCAGAACATTCATTAATAAGTGA 99255
QY 121 CCAATCAGATAGTCTCTGTCCTCCGAATATAGAGCTAGAGCTAGTGTCTTGTCTCAAGATA 180
DB 99256 CCAATCAGTGTCTCTGTCCTCCGAATATAGAGCTAGAGCTAGTGTCTTGTCTCAAGATA 99315
QY 181 CATGCTTGAGATTTTACATTCACCCCCCTAGACACACTCTTAAGACACAACTTAAAGAC 240
DB 99316 CATGCTTGAGATTTTACATTCACCCCCCTAGACACACTCTTAAGACACAACTTAAAGAC 99375
QY 241 ACCCATGTACATGCCCTAA 260
DB 99376 ACCCATGTACATGCCCTAA 99395

RESULT 13
LOCUS ZMGLOSSY
DEFINITION Z.mays Glossy2 locus DNA.
ACCESSION X88779
VERSION X88779.1 GI:949979
KEYWORDS

DNA linear 6343 bp PLN 09-MAY-1996

SOURCE Zea mays
ORGANISM Zea mays

REFERENCE 1
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

TITLE Transposon tagging of the maize Glossy2 locus with the transposable element En/Spm

JOURNAL Plant J. 8 (6), 907-917 (1995)

PMID 8580961

REFERENCE 2 (bases 1 to 6343)
AUTHORS Tacke, E.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-1995) E. Tacke, Max-Planck-Institute, Dept. Salamini, Carl-von-Linne-Weg 10, 50829 Koeln, NRW, FRG

FEATURES
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exon
ORIGIN

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Best Local Similarity 93.9%; Pred. No. 3.9e-52;
Matches 247; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

Qy 1 CTGCACGGTACTTCCAAAGTATTAAGACACACAGTCAAAACACCAATATGACGAGTGGTCATGTC 60
Db 3615 CTGCACGGTACTTCCAAAGTATTAAGACACACACTTAAACACATATATACATGAGTGGTCATATC 3674

Qy 61 TAAACATGTCGTCCTTACCATATTCATTTGATCAATCAAGACACATTCATCAATTAAGTGA 120
Db 3675 TAAACATGTCGTCCTTACCATATTTATTTACCAATCAGGCGATTCATTAATTAAGTGA 3734

Qy 121 CCAATCAGATGTCCTGTCCTCCGATATAGCTTAGACACTGTGCTTCTGTCAGATTA 180
Db 3735 CCAATCAGATGTCCTGTCCTCGAATATAGAGTCAAGACACCCGTCGTCCTGTCAGATTA 3794

Qy 181 CATGTCCTTGACATTTTTCATCTTACCTTACCCCTTACGACACTCTTAAGACACAACTTAAGAC 240
Db 3795 CATGTCCTTGACATTTTTCATCTTACCTTACCTTCTTACGACACTCTTAAGACACAACTTAAGAC 3854

Qy 241 A-CCATTGTATGCCCTTAACCT 262
Db 3855 ACCCCACGGTACATGCCCTTAACCT 3877

RESULT 14
AC151050
LOCUS
DEFINITION

AC151050 134692 bp DNA linear HTG 03-FEB-2005
Zea mays clone ZMMBc0243P06, *** SEQUENCING IN PROGRESS ***, 14
unordered pieces.

AC151050
AC151050.2 GI:57790152

HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVSEFIN.

KEYWORDS
SOURCE
ORGANISM

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 134692)

Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K. and Messing, J.

Zea mays, clone ZMMBc0243P06

Unpublished

2 (bases 1 to 134692)

Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArelano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rappaport, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (19-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 134692)

Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArelano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rappaport, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (03-FEB-2005) Broad Institute of MIT and Harvard, 320

Charles Street, Cambridge, MA 02141, USA

On Jan 14, 2005 this sequence version replaced gi:51372063.

All repeats were identified using RepeatMasker.

Smit, A.P.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Broad Institute of MIT and Harvard
Center code: WIGR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu

Bharti, AK and Messing, J: The Plant Genome Initiative at
Rutgers, Waksman Institute, Rutgers, The State University of New
Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
(http://pgir.rutgers.edu)
Butler, E and Wing, R: Arizona Genomics Institute, Biological
Sciences West, 448A, P.O. Box 210088, University of Arizona,
Tucson, AZ 85721, USA (http://www.genome.arizona.edu)

----- Project Information

Center project name: L30292
Center clone name: 243_P_6

* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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1 1104: contig of 1104 bp in length
* 1105 1204: gap of unknown length
* 1205 4179: contig of 2975 bp in length
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* 4280 21091: contig of 16812 bp in length
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* 21192 26635: contig of 5444 bp in length
* 26636 26735: gap of unknown length
* 26736 65463: contig of 38728 bp in length
* 65464 65563: gap of unknown length
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* 69590 69689: gap of unknown length
* 69690 75792: contig of 6103 bp in length
* 75793 75892: gap of unknown length
* 75893 78948: contig of 3056 bp in length
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* 81705 81804: gap of unknown length
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* 89600 89699: gap of unknown length
* 89700 95873: contig of 6174 bp in length
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FEATURES

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Best Local Similarity 91.9%; Pred. No. 6.1e-52;
Matches 239; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 2 TGCACGGTACTCCAAAGTATAGACACACAGCTAAACACACATATGAGTGGTCTATGCT 61
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Qy 122 CAATCAGATAGTCTCCGTCCGGAATATAGACTTAAGACACTGTGCTTCGTCAAGTAC 181
Db 57747 CAATCAACTAGTCTTCTGTCTCGAACATACAGCTTAAGACATTGTCTTCGTCAAGTAC 57806
Qy 182 ATGCTTTGAGATTTTTTACATTTACACCCCTTAGACACACTCTTAGACACAACTTAAGACA 241
Db 57807 ATGCTTTGAGTTTTTTTACATTTACATTCCTCCGCTAGACACACTCGAAGACACAACTCAAACA 57866
Qy 242 CCCATTGTACATGCCCTTAAC 261
Db 57867 CCCATTGTACATGCCCTTAAC 57886

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RESULT 15

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AC145389
LOCUS
DEFINITION
  Zea mays clone ZMMBBc0054A01, *** SEQUENCING IN PROGRESS ***, 4
  ordered pieces.
AC145389
VERSION
  AC145389.6 GI:48762556
KEYWORDS
  HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE
  Zea mays
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
  Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
  1 (bases 1 to 198102)
  Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.
  and Messing, J.
  Zea mays, clone ZMMBBc0054A01
  Unpublished
  TITLE
  Zea mays, clone ZMMBBc0054A01
  JOURNAL
  2 (bases 1 to 198102)
  Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
  Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
  Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
  Collymore, A., Cooke, P., Corum, B., Dearellano, K.,
  Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
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  Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
  Kamat, A., Karatas, A., Kellis, C., Landers, T., Levine, R.,
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  Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
  Meldrim, J., Meneus, J., Mihova, T., Miens, V., Murphy, T., Naylor, J.,
  Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
  O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

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Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (01-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 198102)

REFERENCE

AUTHORS

Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A. K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArelano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., MacLean, C., MacDonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melidrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (20-JUN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jun 16, 2004 this sequence version replaced gi:48717652.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

TITLE

JOURNAL

COMMENT

Center: Whitehead Institute/MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@broad.mit.edu

Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA (<http://pgir.rutgers.edu>)

Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (<http://www.genome.arizona.edu>)

----- Project Information

Center project name: L29613

Center clone name: 54.A.1

----- Consensus Information

This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Q20 or manually edited. This assembly was performed with Phrap. All trace files for this project are available at the NCBI trace repository (<http://www.ncbi.nlm.nih.gov/Traces/trace.fcgi?>). An exact list of reads used in this assembly are available at <http://www.broad.mit.edu/annotation/plants/maize/randomclones.html>.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 20266: contig of 20266 bp in length

* 20267 20366: gap of 100 bp

* 20367 78634: contig of 58268 bp in length

* 78635 78734: gap of 100 bp

* 78735 140318: contig of 61584 bp in length

* 140319 140418: gap of 100 bp

* 140419 198102: contig of 57684 bp in length.

FEATURES

source

1. 198102

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="B73"

/db_xref="taxon:4577"

/clone_lib="CHORI-201 Maize B73 BAC EORI Library"

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/estimated_length=100

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/estimated_length=100

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Matches 248; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

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QY 182 ATGCTTTGAGATTTTTTACATTCACCCCTTAGACACACATCTTAAGACACAACTTTAAGACA 241
DB 173658 GTGCTTTGAGATTTTTTACATTCACCCCTTAGACACACATCTTAAGACACAACTTTAAGACA 173717

QY 242 CCCATTGTATGCGCCCTTAATCGGACCGCTAC 273
DB 173718 CCCACTGTACATGCGCCCTTAGAGCTGCCGGTGC 173749

Search completed: March 5, 2006, 11:12:25
Job time : 4265 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocellera Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 11:24:36 ; Search time 862 Seconds
(without alignments)
7895.241 Million cell updates/sec

Title: US-10-660-208-90

Perfect score: 823

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Scoring table: 

Gapop 60.0, Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA Main:

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- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	823	100.0	823	7	US-10-660-208-90
3	473	57.5	1587	3	US-09-846-903-87
4	473	57.5	1587	7	US-10-660-208-87
5	75	9.1	875	8	US-10-425-115-13667
6	75	9.1	1251	8	US-10-425-115-13680
7	73	8.9	859	8	US-10-425-115-13670
8	70	8.5	836	8	US-10-425-115-13673
9	66	8.0	894	8	US-10-425-115-13677
10	63	7.7	485	7	US-10-425-114-23949
11	63	7.7	814	8	US-10-425-115-134827
12	62	7.5	821	7	US-10-425-114-16472
13	59	7.2	791	7	US-10-425-114-12914
14	59	7.2	795	7	US-10-425-114-12891
15	49	6.0	178	8	US-10-425-115-39694
16	49	6.0	781	7	US-10-425-114-16676
17	47	5.7	651	8	US-10-425-115-134827
18	44	5.3	379	8	US-10-425-115-34629
19	40	4.9	307	3	US-09-234-0938-6065
20	40	4.9	1326	7	US-10-425-114-31817
21	40	4.9	2760	8	US-10-425-115-69837
22	36	4.4	782	7	US-10-425-114-16647
23	36	4.4	1578	7	US-10-425-114-22826

24	35	4.3	845	8	US-10-425-115-3355	Sequence 3355, Ap
25	32	3.9	6550	7	US-10-759-602-1	GENERAL INFORMA
26	32	3.9	9299	7	US-10-759-602-15	Sequence 15, Appl
27	32	3.9	9408	7	US-10-759-602-16	Sequence 16, Appl
28	30	3.6	720	3	US-09-950-933A-8	Sequence 8, Appl
29	30	3.6	737	7	US-10-425-114-27876	Sequence 27876, A
30	30	3.6	802	8	US-10-425-115-16797	Sequence 36797, A
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ALIGNMENTS

RESULT 1
US-09-846-903-90
; Sequence 90, Application US/09846903
; Publication No. US20030200565A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; TITLE OF INVENTION: OF GENE EXPRESSION
; FILE REFERENCE: 38-21(15678)B Promoters
; CURRENT APPLICATION NUMBER: US/09/846,903
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/201,255
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 90
; LENGTH: 823
; TYPE: DNA
; ORGANISM: Zea mays
US-09-846-903-90

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			Indels	0;
			Gaps	0;
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Db 721 ATATACACAGACGACGATACCATATCGTGTGTAGAGCAACTGAAACAGCCGAGC 780
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RESULT 2
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; Sequence 90, Application US/10660208
; Publication No. US20040133946A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; FILE REFERENCE: 38-21(15678)B promoters
; CURRENT APPLICATION NUMBER: US/10/660,208
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 60/201,255
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 90
; TYPE: DNA
; ORGANISM: Zea mays
US-10-660-208-90

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CTGACGGTACTCCAAAGTATAGACACAGCTAAACACAACTATGCGAGTGTATGTC 60
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Qy 781 GATCTCTCTCCCTCTCCCTCTCCGATCCATTCCTCAGCGCAG 823
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RESULT 3
US-09-846-903-87
; Sequence 87, Application US/09846903
; Publication No. US20030200565A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; FILE REFERENCE: 38-21(15678)B promoters
; CURRENT APPLICATION NUMBER: US/09/846,903
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/201,255
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 87
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Zea mays

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US-09-846-903-87

Query Match 57.5%; Score 473; DB 3; Length 1587;

Best Local Similarity 100.0%; Pred. No. 3.6e-251; Indels 0; Gaps 0;

Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 471 CAGAAGTATTCGTGCTGCATATTCGTAATTTATAGCGAGGCGCCACAGGCCCATCTTC 530

DB 1211 CAGAAGTATTCGTGCTGCATATTCGTAATTTATAGCGAGGCGCCACAGGCCCATCTTC 1270

QY 531 ACTTCGAGGTGAGCATTCGTTTGTAAAGTCTTCGATAAATTTGTTCACTTAAATAG 590

DB 1271 ACTTCGAGGTGAGCATTCGTTTGTAAAGTCTTCGATAAATTTGTTCACTTAAATAG 1330

QY 591 ACCAGTTCAATTCGTGTTAGTCAACATGCTGATCCACGGGGAGCGAGGAGCGAA 650

DB 1331 ACCAGTTCAATTCGTGTTAGTCAACATGCTGATCCACGGGGAGCGAGGAGCGAA 1390

QY 651 TGTGTGCGCCGCGAGTGGCCAGCGAGCGCGGTCGTCGTCACCAACCCCTCG 710

DB 1391 TGTGTGCGCCGCGAGTGGCCAGCGAGCGCGGTCGTCGTCACCAACCCCTCG 1450

QY 711 TTTATACATATATACACAGCGACGATACCCATATCGTGGTGTAGAAGCAACTGAAA 770

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DB 1511 ACAGCGAGCGATCTCTCTCCCTCTCCGATCCCATTTCTCCAGCGCGAG 1563

RESULT 4

US-10-660-208-87

; Sequence 87, Application US/10660208

; Publication No. US20040133946A1

; GENERAL INFORMATION:

; APPLICANT: Conner, Timothy W.

; APPLICANT: Dubois, Patrice

; APPLICANT: Malven, Marianne

; APPLICANT: Masucci, James D.

; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL

; FILE REFERENCE: 38-21(15878)B promoters

; CURRENT APPLICATION NUMBER: US/10/660,208

; PRIOR FILING DATE: 2003-09-11

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 87

; LENGTH: 1587

; TYPE: DNA

; ORGANISM: Zea mays

US-10-660-208-87

Query Match 57.5%; Score 473; DB 7; Length 1587;

Best Local Similarity 100.0%; Pred. No. 3.6e-251;

Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1091 TTTAGACTGATGCGAGTGCATTCATAGAGCAAAAACAGTGTAGAAGCCGTATAAGCAT 1150

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DB 1151 TAAGCAAAACAGCGCAATTCGTAGCTAACACCAATTTGCTGGCTTCCATGGGCATCG 1210

QY 471 CAGAAGTATTCGTGCTGCATATTCGTAATTTATAGCGAGGCGCCACAGGCCCATCTTC 530

DB 1211 CAGAAGTATTCGTGCTGCATATTCGTAATTTATAGCGAGGCGCCACAGGCCCATCTTC 1270

QY 531 ACTTCGAGGTGAGCATTCGTTTGTAAAGTCTTCGATAAATTTGTTCACTTAAATAG 590

DB 1271 ACTTCGAGGTGAGCATTCGTTTGTAAAGTCTTCGATAAATTTGTTCACTTAAATAG 1330

QY 591 ACCAGTTCAATTCGTGTTAGTCAACATGCTGATCCACGGGGAGCGAGGAGCGAA 650

DB 1331 ACCAGTTCAATTCGTGTTAGTCAACATGCTGATCCACGGGGAGCGAGGAGCGAA 1390

QY 651 TGTGTGCGCCGCGAGTGGCCAGCGAGCGCGGTCGTCGTCACCAACCCCTCG 710

DB 1391 TGTGTGCGCCGCGAGTGGCCAGCGAGCGCGGTCGTCGTCACCAACCCCTCG 1450

QY 711 TTTATACATATATACACAGCGACGATACCCATATCGTGGTGTAGAAGCAACTGAAA 770

DB 1451 TTTATACATATATACACAGCGACGATACCCATATCGTGGTGTAGAAGCAACTGAAA 1510

QY 771 ACAGCGAGCGATCTCTCTCCCTCTCCGATCCCATTTCTCCAGCGCGAG 823

DB 1511 ACAGCGAGCGATCTCTCTCCCTCTCCGATCCCATTTCTCCAGCGCGAG 1563

RESULT 5

US-10-425-115-13667

; Sequence 13667, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 13667

; LENGTH: 875

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_112455C.1

US-10-425-115-13667

Query Match 9.1%; Score 75; DB 8; Length 875;

Best Local Similarity 100.0%; Pred. No. 2.6e-30;

Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 749 GTGGTGTCTAGAACCACTGAAAACAGCGAGCGATCTCTCTCCCTCTCCCGATC 808

DB 25 GTGGTGTCTAGAACCACTGAAAACAGCGAGCGATCTCTCTCCCTCTCCCGATC 84

QY 809 CATTCTCCAGCGCGAG 823

DB 85 CATTCTCCAGCGCGAG 99

RESULT 6

US-10-425-115-13680

; Sequence 13680, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With


```
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13680
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112467C.1
US-10-425-115-13680

Query Match      9.1%; Score 75; DB 8; Length 1251;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 749 GTGGTGCTAGAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCGATC 808
Db 371 GTGGTGCTAGAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCGATC 430

Qy 809 CATTCTCCAGCGCAG 823
Db 431 CATTCTCCAGCGCAG 445

RESULT 7
US-10-425-115-13670
; Sequence 13670, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13670
; LENGTH: 859
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112458C.1
US-10-425-115-13670

Query Match      8.9%; Score 73; DB 8; Length 859;
Best Local Similarity 100.0%; Pred. No. 3.3e-29;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 751 GTGTCTAGAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCGATCCA 810
Db 10 GTGTCTAGAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCGATCCA 69

Qy 811 TTCTCCAGCGCAG 823
Db 70 TTCTCCAGCGCAG 82

RESULT 8
US-10-425-115-13673
; Sequence 13673, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13673
; LENGTH: 836
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112460C.1
US-10-425-115-13673

Query Match      8.5%; Score 70; DB 8; Length 836;
Best Local Similarity 100.0%; Pred. No. 1.5e-27;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 754 GCTAGAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCGATCCA 813
Db 10 GCTAGAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCGATCCA 69

Qy 814 TCCAGCGCAG 823
Db 70 TCCAGCGCAG 79

RESULT 9
US-10-425-115-13677
; Sequence 13677, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13677
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112464C.1
US-10-425-115-13677

Query Match      8.0%; Score 66; DB 8; Length 894;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 758 GAAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCGATCCA 817
Db 12 GAAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCGATCCA 71

Qy 818 GCGCAG 823
Db 72 GCGCAG 77

RESULT 10
US-10-425-114-23949/c
; Sequence 23949, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
```


; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 23949

; LENGTH: 485

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3606-031-G10_FLI

US-10-425-114-23949

Query Match 7.7%; Score 63; DB 7; Length 485;

Best Local Similarity 100.0%; Pred. No. 1.1e-23;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 TGTCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGACAC 242

Db 362 TGTCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGACAC 303

Qy 243 CCA 245

Db 302 CCA 300

RESULT 11

US-10-425-115-134827/c

; Sequence 134827, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 134827

; LENGTH: 814

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MET4577_54445C.1

US-10-425-115-134827

Query Match 7.7%; Score 63; DB 8; Length 814;

Best Local Similarity 100.0%; Pred. No. 1.2e-23;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 TGTCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGACAC 242

Db 690 TGTCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGACAC 631

Qy 243 CCA 245

Db 630 CCA 628

RESULT 12

US-10-425-114-16472

; Sequence 16472, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 16472

; LENGTH: 821

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3066-004-E5_FLI

US-10-425-114-16472

Query Match 7.5%; Score 62; DB 7; Length 821;

Best Local Similarity 100.0%; Pred. No. 4.2e-23;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 762 CAACTGAAAACAGCCGAGCGATCTCTCCCTCTCCGATCCATTCACGCGC 821

Db 1 CAACTGAAAACAGCCGAGCGATCTCTCCCTCTCCGATCCATTCACGCGC 60

Qy 822 AG 823

Db 61 AG 62

RESULT 13

US-10-425-114-12914

; Sequence 12914, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 12914

; LENGTH: 791

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: CC-ZMPO148069D04_FLI

US-10-425-114-12914

Query Match 7.2%; Score 59; DB 7; Length 791;

Best Local Similarity 100.0%; Pred. No. 1.9e-21;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 765 CTGAAAACAGCCGAGCGATCTCTCCCTCTCCGATCCATTCACGCGC 823

Db 1 CTGAAAACAGCCGAGCGATCTCTCCCTCTCCGATCCATTCACGCGC 59

RESULT 14

US-10-425-114-12891

; Sequence 12891, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

;; FILE REFERENCE: 38-21(53313)B

;; CURRENT APPLICATION NUMBER: US/10/425,114

;; CURRENT FILING DATE: 2003-04-28

;; NUMBER OF SEQ ID NOS: 73128

;; SEQ ID NO 12891

;; LENGTH: 795

;; TYPE: DNA

;; ORGANISM: Zea mays

;; FEATURE:

;; OTHER INFORMATION: Clone ID: CC-ZMPO148038E03_FLI

US-10-425-114-12891

Query Match

Best Local Similarity 7.2%; Score 59; DB 7; Length 795;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 765 CTGAAACAGCGCGGATCTCTCCCTCTCCGATCCATTCGAGCGAG 823

Db 1 CTGAAACAGCGCGGATCTCTCCCTCTCCGATCCATTCGAGCGAG 59

RESULT 15

US-10-425-115-39694

;; Sequence 39694, Application US/10425115

;; Publication No. US20040214272A1

;; GENERAL INFORMATION:

;; APPLICANT: La Rosa, Thomas J.

;; APPLICANT: Kovalic, David K.

;; APPLICANT: Zhou, Yihua

;; APPLICANT: Cao, Yongwei

;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

;; FILE REFERENCE: 38-21(53222)B

;; CURRENT APPLICATION NUMBER: US/10/425,115

;; CURRENT FILING DATE: 2003-04-28

;; NUMBER OF SEQ ID NOS: 369326

;; SEQ ID NO 39694

;; LENGTH: 178

;; TYPE: DNA

;; ORGANISM: Zea mays

;; FEATURE:

;; NAME/KEY: unsure

;; LOCATION: (1)..(178)

;; OTHER INFORMATION: unsure at all n locations

;; FEATURE:

;; OTHER INFORMATION: Clone ID: MRT4577_136201C.1

US-10-425-115-39694

Query Match

Best Local Similarity 6.0%; Score 49; DB 8; Length 178;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 759 AAGCACTGAAACAGCGGATCTCTCCCTCTCCGATCCATTCGAGCGAG 807

Db 18 AAGCACTGAAACAGCGGATCTCTCCCTCTCCGATCCATTCGAGCGAG 66

Search completed: March 5, 2006, 11:39:06

Job time : 862 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 11:26:37 ; Search time 509 Seconds
(without alignments)
3545.020 Million cell updates/sec

Title: US-10-660-208-90

Perfect score: 823

Sequence: 1 ctgacggtactccaagtat.....cgatccattctccagcgag 823

Scoring table: ONIGONUC
Gapop 60.0, Gapext 60.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA New:

- 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq*
- 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq*
- 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
- 6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
- 7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
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- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	2.7	1471	6	US-09-925-065A-35755
C 2	22	2.7	1617	6	US-09-925-065A-66476
C 3	22	2.7	1617	6	US-09-925-065A-66477
C 4	21	2.6	201	12	US-11-124-367A-26025
C 5	21	2.6	201	12	US-11-124-367A-26026
C 6	21	2.6	610	6	US-09-925-065A-546671
C 7	21	2.6	75782	7	US-10-330-773-772
C 8	21	2.6	390183	7	US-10-330-773-937
C 9	20	2.4	43103	8	US-10-995-561-13346
C 10	20	2.4	71207	7	US-10-330-773-416
C 11	20	2.4	100000	12	US-11-124-367A-5048
C 12	20	2.4	171936	8	US-10-933-025-24
C 13	20	2.4	194186	7	US-10-330-773-395
C 14	19	2.3	23	8	US-10-310-914A-1382480
C 15	19	2.3	201	8	US-10-995-561-17794
C 16	19	2.3	201	8	US-10-995-561-17868
C 17	19	2.3	201	8	US-10-995-561-18020
C 18	19	2.3	201	12	US-11-124-367A-17737
C 19	19	2.3	201	12	US-11-124-367A-17738
C 20	19	2.3	201	12	US-11-124-367A-24462

21	19	2.3	201	12	US-11-124-367A-24839	Sequence 24839, A
22	19	2.3	201	12	US-11-124-367A-25079	Sequence 25079, A
23	19	2.3	413	6	US-09-925-065A-4974	Sequence 4974, Ap
C 24	19	2.3	491	6	US-09-925-065A-917593	Sequence 917593,
C 25	19	2.3	491	6	US-09-925-065A-917594	Sequence 917594,
C 26	19	2.3	494	6	US-09-925-065A-141505	Sequence 141505,
C 27	19	2.3	497	6	US-09-925-065A-327497	Sequence 327497,
C 28	19	2.3	500	6	US-09-925-065A-930919	Sequence 930919,
29	19	2.3	503	6	US-09-925-065A-746493	Sequence 746493,
30	19	2.3	525	6	US-09-925-065A-796124	Sequence 796124,
31	19	2.3	527	6	US-09-925-065A-254418	Sequence 254418,
32	19	2.3	527	6	US-09-925-065A-254419	Sequence 254419,
33	19	2.3	537	6	US-09-925-065A-787721	Sequence 787721,
34	19	2.3	541	6	US-09-925-065A-168639	Sequence 168639,
C 35	19	2.3	544	6	US-09-925-065A-570511	Sequence 570511,
36	19	2.3	549	6	US-09-925-065A-20117	Sequence 20117, A
C 37	19	2.3	553	6	US-09-925-065A-141509	Sequence 141509,
C 38	19	2.3	554	6	US-09-925-065A-21876	Sequence 21876, A
C 39	19	2.3	560	6	US-09-925-065A-939827	Sequence 939827,
C 40	19	2.3	560	6	US-09-925-065A-939828	Sequence 939828,
41	19	2.3	561	6	US-09-925-065A-413845	Sequence 413845,
42	19	2.3	563	6	US-09-925-065A-793626	Sequence 793626,
C 43	19	2.3	566	6	US-09-925-065A-653866	Sequence 653866,
C 44	19	2.3	570	6	US-09-925-065A-732177	Sequence 732177,
C 45	19	2.3	570	6	US-09-925-065A-811564	Sequence 811564,

ALIGNMENTS

RESULT 1
US-09-925-065A-35755/c
; Sequence 35755, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35755
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-35755

Query Match 2.7% Score 22; DB 6; Length 1471;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 783 TCTCTCTCTCTCTCTCTCTCTCC 804
|||||
Db 237 TCTCTCTCTCTCTCTCTCTCTCC 216

RESULT 2
US-09-925-065A-66476/c
; Sequence 66476, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108927.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66476
LENGTH: 1617
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-66476

Query Match 2.7%; Score 22; DB 6; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 783 TCTCTCTCCCTCTCCCTCTCC 804
DB 331 TCTCTCTCCCTCTCCCTCTCC 310

RESULT 3

US-09-925-065A-66477/c
Sequence 66477, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108927.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66477
LENGTH: 1617
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-66477

Query Match 2.7%; Score 22; DB 6; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 783 TCTCTCTCCCTCTCCCTCTCC 804
DB 331 TCTCTCTCCCTCTCCCTCTCC 310

RESULT 4

US-11-124-367A-26025/c

Sequence 26025, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
TITLE OF INVENTION: Genetic Polymorphisms Associated with
FILE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
PRIOR FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26025
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-367A-26025

Query Match 2.6%; Score 21; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 784 CTCCTCTCCCTCTCCCTCTCC 804
DB 24 CTCCTCTCCCTCTCCCTCTCC 4

RESULT 5

US-11-124-367A-26026/c
Sequence 26026, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:

APPLICANT: Michele Cargill
TITLE OF INVENTION: Genetic Polymorphisms Associated with
FILE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
PRIOR FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26026
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-367A-26026

Query Match 2.6%; Score 21; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 784 CTCCTCTCCCTCTCCCTCTCC 804
DB 169 CTCCTCTCCCTCTCCCTCTCC 149

RESULT 6

US-09-925-065A-546671/c
Sequence 546671, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 546671
LENGTH: 610
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-546671

Query Match 2.6%; Score 21; DB 6; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 785 TCCTCTCCCTCTCCCTCTCCG 805
Db 548 TCCTCTCCCTCTCCCTCTCCG 528

RESULT 7
US-10-330-773-772/c
Sequence 772, Application US/10330773
Publication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 772
LENGTH: 75782
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(75782)
OTHER INFORMATION: n = A,T,C or G
US-10-330-773-772

Query Match 2.6%; Score 21; DB 7; Length 75782;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 783 TCCTCTCTCCCTCTCCCTCTC 803
Db 22976 TCCTCTCTCCCTCTCCCTCTC 22956

RESULT 8
US-10-330-773-937/c
Sequence 937, Application US/10330773
Publication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Compositions and Methods in Cancer

FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 937
LENGTH: 390183
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(390183)
OTHER INFORMATION: n = A,T,C or G
US-10-330-773-937

Query Match 2.6%; Score 21; DB 7; Length 390183;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 784 CTCCTCTCCCTCTCCCTCTCC 804
Db 132970 CTCCTCTCCCTCTCCCTCTCC 132950

RESULT 9
US-10-995-561-13346
Sequence 13346, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13346
LENGTH: 43103
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-13346

Query Match 2.4%; Score 20; DB 8; Length 43103;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 785 TCCTCTCCCTCTCCCTCTCC 804
Db 37839 TCCTCTCCCTCTCCCTCTCC 37858

RESULT 10
US-10-330-773-416/c
Sequence 416, Application US/10330773
Publication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 416
LENGTH: 71207
TYPE: DNA
ORGANISM: Homo sapiens
US-10-330-773-416

Query Match 2.4%; Score 20; DB 7; Length 71207;

Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 785 TCCTCTCCCTCTCCCTCTCC 804
DB 37377 TCCTCTCCCTCTCCCTCTCC 37358

RESULT 11
US-11-124-367A-5048/c
; Sequence 5048, Application US/11124367A.
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5048
; LENGTH: 100000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-5048

Query Match 2.4%; Score 20; DB 12; Length 100000;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 786 CCTCTCCCTCTCCCTCTCCG 805
DB 46014 CCTCTCCCTCTCCCTCTCCG 45995

RESULT 12
US-10-933-025-24/c
; Sequence 24, Application US/10933025
; Publication No. US20050265987A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, STEVEN
; APPLICANT: HEMMERICH, STEFAN
; APPLICANT: TOMITA, MEGUMI
; TITLE OF INVENTION: Sulfotransferases and methods of use
; TITLE OF INVENTION: thereof
; FILE REFERENCE: UCAL-230CON
; CURRENT APPLICATION NUMBER: US/10/933,025
; CURRENT FILING DATE: 2004-09-01
; PRIOR APPLICATION NUMBER: 10/025,966
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/258,577
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/267,831
; PRIOR FILING DATE: 2001-09-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 171936
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-933-025-24

Query Match 2.4%; Score 20; DB 8; Length 171936;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 785 TCCTCTCCCTCTCCCTCTCC 804
DB 33 TCCTCTCCCTCTCCCTCTCC 14

RESULT 13
US-10-330-773-395/c
; Sequence 395, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 395
; LENGTH: 194186
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) _ (194186)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-395

Query Match 2.4%; Score 20; DB 7; Length 194186;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 785 TCCTCTCCCTCTCCCTCTCC 804
DB 99078 TCCTCTCCCTCTCCCTCTCC 99059

RESULT 14
US-10-310-914A-1382480/c
; Sequence 1382480, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1382480
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1382480

Query Match 2.3%; Score 19; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 786 CCTCTCCCTCTCCCTCTCC 804
DB 22 CCTCTCCCTCTCCCTCTCC 4

RESULT 15
US-10-995-561-17794
; Sequence 17794, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.

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; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17794
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-17794

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Query Match      2.3%; Score 19; DB 8; Length 201;
Best Local Similarity 100.0%; Pred.No. 6.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 786 CCTCTCCCTCTCCCTCTCC 804
    |||||
Db 169 CCTCTCCCTCTCCCTCTCC 187

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Search completed: March 5, 2006, 11:44:32
Job time : 511 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 11:20:48 ; Search time 4129 Seconds
(without alignments)
9325.689 Million cell updates/sec

Title: US-10-660-208-90

Perfect score: 823

Sequence: 1 ctgacggtactccaagtat.....cgatccattctccagcgag 823

Scoring parameters: Gapop 60.0, Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
- 9: gb_est9.*
- 10: gb_est10.*
- 11: gb_est11.*

Pred. No. is the number of results predicted by the chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	473	57.5	901	10	CG011145
2	169	20.5	815	9	CC409846
3	125	15.2	964	9	CC331498
4	103	12.5	679	9	CC331420
5	103	12.5	894	9	CC356660
6	102	12.4	882	10	CG130321
7	102	12.4	1015	10	CG130320
8	97	11.8	893	10	CG2362236
9	85	10.3	324	9	CC007924
10	83	10.1	737	9	CC409551
11	80	9.7	563	2	BE510330
12	79	9.6	695	10	CW007582
13	79	9.6	777	10	CW006373
14	79	9.6	902	9	CC334197
15	79	9.6	902	9	CC607552
16	76	9.2	847	10	CW009430
17	76	9.2	863	10	CG175756
18	75	9.1	291	6	CF008956
19	75	9.1	534	6	CF010755
20	74	9.0	234	5	BU098918
21	70	8.5	530	6	CF008799
22	70	8.5	649	6	CF011104

23	69	8.4	560	2	BE644379	BE644379	945060F06
24	68	8.3	587	9	CC033608	CC033608	3591-1-64
25	67	8.3	595	5	CC033463	CC033463	3591-1-64
26	67	8.1	294	5	BU097711	BU097711	3524-1-45
27	67	8.1	558	6	CA826767	CA826767	1114004F0
28	67	8.1	606	1	AW499193	AW499193	660043F05
29	67	8.1	612	5	BO485904	BO485904	3524-1-9
30	67	8.1	905	10	CG065264	CG065264	PURFO72TD
31	65	7.9	617	1	AW428651	AW428651	660040H05
32	65	7.9	868	9	BZ817311	BZ817311	PUGCL66TB
33	65	7.9	985	9	BZ817308	BZ817308	PUGCL66TB
34	64	7.8	311	10	CL262067	CL262067	ZMMBB061
35	64	7.8	520	5	BQ528252	BQ528252	3524-1-2
36	64	7.8	530	5	BQ528654	BQ528654	3524-1-35
37	64	7.8	534	5	BQ577582	BQ577582	3524-1-38
38	64	7.8	574	5	BQ528264	BQ528264	3524-1-2
39	64	7.8	588	1	AW499212	AW499212	660043H02
40	64	7.8	611	5	BQ577641	BQ577641	3524-1-39
41	63	7.7	532	5	BU099109	BU099109	3524-1-3
42	63	7.7	544	1	AI833884	AI833884	605096G02
43	63	7.7	635	10	CG119014	CG119014	PUBBF49TB
44	63	7.7	640	1	AW497918	AW497918	660041G02
45	63	7.7	717	9	CC397968	CC397968	PURDC37TD

ALIGNMENTS

RESULT 1
CG011145
LOCUS
ZUAGI45TH ZM 3.0 4.0 KB Zea mays genomic clone ZMMBPa0060H17,
genomic survey sequence.
CG011145
ACCESSION
CG011145.1 GI:33883311
VERSION
GSS.
KEYWORDS
Zea mays
SOURCE
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 901)
AUTHORS
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
TITLE
Consortium for Maize Genomics
JOURNAL
Unpublished (2002)
COMMENT
Other GSSs: ZUAGI45TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
FEATURES
Location/Qualifiers
1..901
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/clone="ZMMBPa0060H17"
/clone_lib="ZM 3.0 4.0 KB"
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genomic DNA library"

ORIGIN
Query Match 57.5%; Score 473; DB 10; Length 901;
Best Local Similarity 100.0%; Pred. No. 1.2e-251;
Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 351 TTAGACTGATGACGCTGCATTTCATAGACAAAACAGTGTAGAGCCGTATAGCAT 410


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CC331420
LOCUS       CC331420                679 bp    DNA        linear    GSS 16-MAY-2003
DEFINITION   OGMK41TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZM5BMA0384G09,
              genomic survey sequence.
ACCESSION    CC331420
VERSION      CC331420.1   GI:30800591
KEYWORDS     GSS.
SOURCE       Zea mays
ORGANISM     Zea mays
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              /db_xref="taxon:4577"
              /clone="ZM5BMA0384G09"
              /clone_lib="ZM 0.7_1.5_KB"
              /notes="Vector: pCR4-TOPO; Site 1: HincII; 0.7-1.5 kb
              methylation filtered genomic DNA library"

REFERENCE
AUTHORS      Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
              Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
              Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
              Consortium for Maize Genomics
              Unpublished (2003)
              Contact: Cathy Whitelaw
              TIGR
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301-838-5843
              Fax: 301-838-0208
              Email: whitelaw@tigr.org
              Seq primer: TF
              Class: methylation filtered.
              Location/Qualifiers
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                /strain="B73"
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  Best Local Similarity 100.0%; Pred. No. 2.2e-45;
  Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

  Oy 143 CGAATATAGAGCTAAGACACTGTCTCTCGTCAAGATACATGCTTCGAGATTTTACAT 202
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  Db 260 CGAATATAGAGCTAAGACACTGTCTCTCGTCAAGATACATGCTTCGAGATTTTACAT 319
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  Oy 203 TCACCCCTAGACACACTCTTAAGACACAACTTAAGACACCCA 245
        |||||||
  Db 320 TCACCCCTAGACACACTCTTAAGACACAACTTAAGACACCCA 362
        |||||||

RESULT 5
CC356660/c
LOCUS       CC356660                894 bp    DNA        linear    GSS 16-MAY-2003
DEFINITION   PUHQ61TD_ZM_0.6_1.0_KB_Zea_mays_genomic_clone_ZM5BTA513L02,
              genomic survey sequence.
ACCESSION    CC356660
VERSION      CC356660.1   GI:30826060
KEYWORDS     GSS.
SOURCE       Zea mays
ORGANISM     Zea mays
              /organism="Zea mays"
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              /strain="B73"
              /db_xref="taxon:4577"
              /clone="ZM5BTA0794H17"
              /clone_lib="ZM 0.6_1.0_KB"
              /notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
              Cot selected genomic DNA library"

REFERENCE
AUTHORS      Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
              Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
              Bennetzen,J.
              Maize Genomics Consortium
              Unpublished (2003)
              Contact: Cathy Whitelaw
              TIGR
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301-838-5843
              Fax: 301-838-0208
              Email: whitelaw@tigr.org
              Seq primer: TF
              Class: sheared ends.
              Location/Qualifiers
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                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="B73"
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                /clone="ZM5BTA0794H17"
                /clone_lib="ZM 0.6_1.0_KB"
                /notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
                Cot selected genomic DNA library"

CoT selected genomic DNA library"

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```

Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
      Location/Qualifiers
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        /organism="Zea mays"
        /mol_type="genomic DNA"
        /strain="B73"
        /db_xref="taxon:4577"
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        /notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
        CoT selected genomic DNA library"

ORIGIN
Query Match       12.5%; Score 103; DB 9; Length 894;
Best Local Similarity 100.0%; Pred. No. 2.2e-45;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

.Oy 143 CGAATATAGAGCTAAGACACTGTCTCTCGTCAAGATACATGCTTCGAGATTTTACAT 202
        |||||||
Db 131 CGAATATAGAGCTAAGACACTGTCTCTCGTCAAGATACATGCTTCGAGATTTTACAT 72
        |||||||

Oy 203 TCACCCCTAGACACACTCTTAAGACACAACTTAAGACACCCA 245
        |||||||
Db 71 TCACCCCTAGACACACTCTTAAGACACAACTTAAGACACCCA 29
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RESULT 6
CG130321
LOCUS       PUKDM45TD_ZM_0.6_1.0_KB_Zea_mays_genomic_clone_ZM5BTA0794H17,
              genomic survey sequence.
ACCESSION    CG130321
VERSION      CG130321.1   GI:34017768
KEYWORDS     GSS.
SOURCE       Zea mays
ORGANISM     Zea mays
              /organism="Zea mays"
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              /strain="B73"
              /db_xref="taxon:4577"
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              /notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
              Cot selected genomic DNA library"

REFERENCE
AUTHORS      Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
              Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
              Bennetzen,J.
              Maize Genomics Consortium
              Unpublished (2003)
              Other GSSs: PUKDM45TB
              Contact: Cathy Whitelaw
              TIGR
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301-838-5843
              Fax: 301-838-0208
              Email: whitelaw@tigr.org
              Seq primer: TF
              Class: sheared ends.
              Location/Qualifiers
                1..882
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="B73"
                /db_xref="taxon:4577"
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                /notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
                Cot selected genomic DNA library"

CoT selected genomic DNA library"

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REFERENCE 144 GAATATAGAGCTAAGACACTGTGCTTCGTCGAAGATACATGCTTGAGATTTTACATT 203
Db 578 GAATATAGAGCTAAGACACTGTGCTTCGTCGAAGATACATGCTTGAGATTTTACATT 637

Qy 204 CACCCCCCTAGACACACTCTTAAGACACAACTTTAAGACACCCA 245
Db 638 CACCCCCCTAGACACACTCTTAAGACACAACTTTAAGACACCCA 679

RESULT 7
CGI30320/c
LOCUS PUKDM45TB ZM 0.6_1.0_KB DNA linear GSS 21-AUG-2003
DEFINITION genomic survey sequence.
ACCESSION CGI30320
VERSION CGI30320
KEYWORDS GSS.
SOURCE Zea mays

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1015)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other_GSSs: PUKDM45TD
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
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Cot selected genomic DNA library"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.9e-45;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 144 GAATATAGAGCTAAGACACTGTGCTTCGTCGAAGATACATGCTTGAGATTTTACATT 203
Db 849 GAATATAGAGCTAAGACACTGTGCTTCGTCGAAGATACATGCTTGAGATTTTACATT 790

Qy 204 CACCCCCCTAGACACACTCTTAAGACACAACTTTAAGACACCCA 245
Db 789 CACCCCCCTAGACACACTCTTAAGACACAACTTTAAGACACCCA 748

RESULT 8
CZ362236/c
LOCUS ZMBF0140018r ZMBF Zea mays genomic clone ZMBF0140018 3', genomic
DEFINITION survey sequence.
ACCESSION CZ362236
VERSION CZ362236
KEYWORDS GSS.
SOURCE Zea mays

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 324)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
source
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Cot selected genomic DNA library"

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Best Local Similarity 100.0%; Pred. No. 4.8e-42;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 CGAATATAGAGCTAAGACACTGTGCTTCGTCGAAGATACATGCTTGAGATTTTACATT 202
Db 307 CGAATATAGAGCTAAGACACTGTGCTTCGTCGAAGATACATGCTTGAGATTTTACATT 248

Qy 203 TCACCCCCCTAGACACACTCTTAAGACACAACTTTAAGA 239
Db 247 TCACCCCCCTAGACACACTCTTAAGACACAACTTTAAGA 211

RESULT 9
CC007924
LOCUS PUBE148TD ZM 0.6_1.0_KB Zea mays genomic clone ZMBF0197H23,
DEFINITION genomic survey sequence.
ACCESSION CC007924
VERSION CC007924.1
KEYWORDS GSS.
SOURCE Zea mays

ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 324)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN
Query Match 11.8%; Score 97; DB 10; Length 893;
Best Local Similarity 100.0%; Pred. No. 4.8e-42;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 CGAATATAGAGCTAAGACACTGTGCTTCGTCGAAGATACATGCTTGAGATTTTACATT 202
Db 307 CGAATATAGAGCTAAGACACTGTGCTTCGTCGAAGATACATGCTTGAGATTTTACATT 248

Qy 203 TCACCCCCCTAGACACACTCTTAAGACACAACTTTAAGA 239
Db 247 TCACCCCCCTAGACACACTCTTAAGACACAACTTTAAGA 211

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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZM 0.6-1.0 KB"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.3e-35;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 ACTGTGCTTCGTCAGATACATGCTTGAGATTTTACATTCACCCCTAGACAC 220
Db 30 ACTGTGCTTCGTCAGATACATGCTTGAGATTTTACATTCACCCCTAGACAC 89

QY 221 TCTAAGACACAACTTAAGACACCA 245
Db 90 TCTAAGACACAACTTAAGACACCA 114

RESULT 10
CC409551/c
LOCUS      737 bp      DNA      linear      GSS 19-MAY-2003
DEFINITION genomic survey sequence.
ACCESSION  CC409551
VERSION    CC409551.1 GI:30889641
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 737)
AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
TITLE      Maize Genomics Consortium
JOURNAL    Unpublished (2003)
COMMENT    Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
FEATURES   Location/Qualifiers
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                        /organism="Zea mays"
                        /mol_type="genomic DNA"
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ORIGIN

Query Match      10.1%; Score 83; DB 9; Length 737;
Best Local Similarity 100.0%; Pred. No. 3.1e-34;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 TGTGCTTCGTCAGATACATGCTTGAGATTTTACATTCACCCCTAGACAC 222
Db 146 TGTGCTTCGTCAGATACATGCTTGAGATTTTACATTCACCCCTAGACAC 87

QY 223 TAAGACACAACTTAAGACACCA 245
Db 86 TAAGACACAACTTAAGACACCA 64

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RESULT 11
BE510330
LOCUS      563 bp      mRNA      linear      EST 07-AUG-2000
DEFINITION 946052B01.x1 946 - tassels primordium prepared by Schmidt lab Zea
            mays cDNA, mRNA sequence.
ACCESSION  BE510330
VERSION    BE510330.1 GI:9731578
KEYWORDS   EST.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 563)
AUTHORS   Walbot,V.
TITLE      Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL    Unpublished (1999)
COMMENT    Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2227
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Plate: 946052 row: B column: 01.
FEATURES   Location/Qualifiers
            source          1..563
                        /organism="Zea mays"
                        /mol_type="mRNA"
                        /cultivar="OH43"
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                        /tissue_type="tassels"
                        /dev_stage="just after the transition from vegetative to
                        inflorescence development"
                        /lab_host="XLOLR"
                        /clone_lib="946 - tassels primordium prepared by Schmidt
                        lab"
                        /note="Organ: tassels; Vector: HybridZAP; Site 1: EcoRI;
                        Site 2: XhoI; George Chuck dissected immature tassels
                        between 1mm and 3mm. Sharon Stanfield prepared the cDNA
                        library in HybridZAP. Sample insert size range was 350 bp
                        to 3 Kb with a 1 Kb average."
ORIGIN

Query Match      9.7%; Score 80; DB 2; Length 563;
Best Local Similarity 100.0%; Pred. No. 1.4e-32;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 CACTGTGCTTCGTCAGATACATGCTTGAGATTTTACATTCACCCCTAGACACA 219
Db 1 CACTGTGCTTCGTCAGATACATGCTTGAGATTTTACATTCACCCCTAGACACA 60

QY 220 CTTAAGACACAACTTAAGA 239
Db 61 CTTAAGACACAACTTAAGA 80

RESULT 12
CW007582
LOCUS      695 bp      DNA      linear      GSS 23-SEP-2004
DEFINITION ZM5BLA0009E11.r ZM5BLA Zea mays genomic clone ZM5BLA0009E11 3',
            genomic survey sequence.
ACCESSION  CW007582
VERSION    CW007582.1 GI:52588391
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.

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DEFINITION OGUEN60TV ZM_0.7-1.5 KB Zea mays genomic clone ZMMBMA0401J24,
genomic survey sequence.
ACCESSION CC607552
VERSION CC607552.1 GI:31968973
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 902)
AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Reanick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other_GSSs: OGUEN60TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
FEATURES
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Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
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/clone="ZMMBMA0401J24"
/clone_lib="ZM 0.7-1.5 KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
ORIGIN
Query Match 9.6%; Score 79; DB 9; Length 902;
Best Local Similarity 100.0%; Pred. No. 5.2e-32;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 143 CGAATATAGACTAAGACACTGTGTTCTCGTCAAGATACATGTTGAGATTTTACAT 202
Db 503 CGAATATAGACTAAGACACTGTGTTCTCGTCAAGATACATGTTGAGATTTTACAT 562
Qy 203 TCACCCCTAGACACT 221
Db 563 TCACCCCTAGACACT 581

Search completed: March 5, 2006, 14:56:37
Job time : 4131 secs

US-08-581-148C-30

Query Match 4.4%; Score 36; DB 3; Length 6343;
Best Local Similarity 100.0%; Pred. No. 3.9e-09;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 CATTCAATAAATTAAGTGACCAATCAGATAGTCCTC 136
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Db 3715 CATTCAATAAATTAAGTGACCAATCAGATAGTCCTC 3750

RESULT 2

US-09-097-319A-1

; Sequence 1, Application US/09097319A

; Patent No. 6384207

; GENERAL INFORMATION:

; APPLICANT: Ainley, Michael

; APPLICANT: Armstrong, Katherine

; APPLICANT: Belmar, Scott

; APPLICANT: Folkerts, Otto

; APPLICANT: Hopkins, Nicole

; APPLICANT: Menke, Michael A.

; APPLICANT: Paredy, Davakar

; APPLICANT: Petolino, Joseph F.

; APPLICANT: Smith, Kelley

; APPLICANT: Woosley, Aaron

; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DowElanco Patent Department

; STREET: 9330 Zionsville Road

; CITY: Indianapolis

; STATE: Indiana

; COUNTRY: USA

; ZIP: 46268

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/097,319A

; FILING DATE:

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Stuart, Donald R

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317 337 4816

; TELEFAX: 317 337 4847

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6550 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; FEATURE:

; NAME/KEY: exon

; LOCATION: 4201..4425

; OTHER INFORMATION: /product= "Peroxidase"

; FEATURE:

; NAME/KEY: intron

; LOCATION: 4426..5058

; FEATURE:

; NAME/KEY: exon

; LOCATION: 5059..5250

; FEATURE:

; NAME/KEY: intron

; LOCATION: 5251..5382

; FEATURE:

; NAME/KEY: exon

; LOCATION: 5383..5548

; FEATURE:

; NAME/KEY: intron

; LOCATION: 5549..5649

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; NAME/KEY: intron

; LOCATION: 5549..5649

; FEATURE:

; NAME/KEY: exon

; LOCATION: 5650..6065

; FEATURE:

; NAME/KEY: CDS

; LOCATION: join(4201..4425, 5059..5250, 5383..5547, 5649

; LOCATION: ..6068)

; US-09-097-319A-1

Query Match 3.9%; Score 32; DB 3; Length 6550;

Best Local Similarity 100.0%; Pred. No. 5.9e-07;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 TCTAAACATGTGCTTACCATATTCATTGTA 90

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Db 1415 TCTAAACATGTGCTTACCATATTCATTGTA 1446

RESULT 3

US-09-643-971-1

; Sequence 1, Application US/09643971

; Patent No. 6699984

; GENERAL INFORMATION:

; APPLICANT: Ainley, Michael

; APPLICANT: Armstrong, Katherine

; APPLICANT: Belmar, Scott

; APPLICANT: Folkerts, Otto

; APPLICANT: Hopkins, Nicole

; APPLICANT: Menke, Michael A.

; APPLICANT: Paredy, Davakar

; APPLICANT: Petolino, Joseph F.

; APPLICANT: Smith, Kelley

; APPLICANT: Woosley, Aaron

; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DowElanco Patent Department

; STREET: 9330 Zionsville Road

; CITY: Indianapolis

; STATE: Indiana

; COUNTRY: USA

; ZIP: 46268

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/643,971

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Stuart, Donald R

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317 337 4816

; TELEFAX: 317 337 4847

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6550 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; FEATURE:

; NAME/KEY: exon

; LOCATION: 4201..4425

; OTHER INFORMATION: /product= "Peroxidase"

; FEATURE:

; NAME/KEY: intron

; LOCATION: 4426..5058

; FEATURE:

NAME/KEY: exon
LOCATION: 5059..5250
FEATURE:
NAME/KEY: intron
LOCATION: 5251..5382
FEATURE:
NAME/KEY: exon
LOCATION: 5383..5548
FEATURE:
NAME/KEY: intron
LOCATION: 5549..5649
FEATURE:
NAME/KEY: exon
LOCATION: 5650..6065
FEATURE:
NAME/KEY: CDS
LOCATION: join(4201..4425, 5059..5250, 5383..5547, 5649
LOCATION: ..6068)
US-09-643-971-1

Query Match 3.9%; Score 32; DB 3; Length 6550;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 TCTAAACATGTGCTTACCATTTCATTGTA 90
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Db 1415 TCTAAACATGTGCTTACCATTTCATTGTA 1446

RESULT 4
US-09-097-319A-15
; Sequence 15, Application US/09097319A
; Patent No. 6384207
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; APPLICANT: Armstrong, Katherine
; APPLICANT: Belmar, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Hopkins, Nicole
; APPLICANT: Menke, Michael A.
; APPLICANT: Paredy, Dayakar
; APPLICANT: Petolino, Joseph F.
; APPLICANT: Smith, Kelley
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dowelanco Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,319A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 4816
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9299 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular

MOLECULE TYPE: DNA
US-09-097-319A-15
Query Match 3.9%; Score 32; DB 3; Length 9299;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 59 TCTAAACATGTGCTTACCATTTCATTGTA 90
|||||
Db 1462 TCTAAACATGTGCTTACCATTTCATTGTA 1493
RESULT 5
US-09-643-971-15
; Sequence 15, Application US/09643971
; Patent No. 6699984
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; APPLICANT: Armstrong, Katherine
; APPLICANT: Belmar, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Hopkins, Nicole
; APPLICANT: Menke, Michael A.
; APPLICANT: Paredy, Dayakar
; APPLICANT: Petolino, Joseph F.
; APPLICANT: Smith, Kelley
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dowelanco Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,971
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 4816
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9299 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
US-09-643-971-15

Query Match 3.9%; Score 32; DB 3; Length 9299;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 TCTAAACATGTGCTTACCATTTCATTGTA 90
|||||
Db 1462 TCTAAACATGTGCTTACCATTTCATTGTA 1493

RESULT 6
US-09-097-319A-16
; Sequence 16, Application US/09097319A
; Patent No. 6384207
; GENERAL INFORMATION:

APPLICANT: Ainley, Michael
APPLICANT: Armstrong, Katherine
APPLICANT: Belmar, Scott
APPLICANT: Folkerts, Otto
APPLICANT: Hopkins, Nicole
APPLICANT: Menke, Michael A.
APPLICANT: Paredy, Dayakar
APPLICANT: Petolino, Joseph F.
APPLICANT: Smith, Kelley
APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dowelanco Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,319A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 9408 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-09-097-319A-16
Query Match 3.9%; Score 32; DB 3; Length 9408;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 59 TCTAAACATGTCCTTACCATTTCATTGTA 90
|||||
Db 1468 TCTAAACATGTCCTTACCATTTCATTGTA 1499
RESULT 7
US-09-643-971-16
Sequence 16, Application US/09643971
Patent No. 669984
GENERAL INFORMATION:
APPLICANT: Ainley, Michael
APPLICANT: Armstrong, Katherine
APPLICANT: Belmar, Scott
APPLICANT: Folkerts, Otto
APPLICANT: Hopkins, Nicole
APPLICANT: Menke, Michael A.
APPLICANT: Paredy, Dayakar
APPLICANT: Petolino, Joseph F.
APPLICANT: Smith, Kelley
APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dowelanco Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana

COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,971
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 9408 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-09-643-971-16
Query Match 3.9%; Score 32; DB 3; Length 9408;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 59 TCTAAACATGTCCTTACCATTTCATTGTA 90
|||||
Db 1468 TCTAAACATGTCCTTACCATTTCATTGTA 1499
RESULT 8
US-09-950-933A-8
Sequence 8, Application US/09950933A
Patent No. 6875907
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro, Pedro
TITLE OF INVENTION: Antimicrobial Peptides and Methods of
TITLE OF INVENTION: Use
FILE REFERENCE: 35718/238472
CURRENT APPLICATION NUMBER: US/09/950,933A
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/232,569
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 720
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (119)....(403)
US-09-950-933A-8
Query Match 3.6%; Score 30; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 48 CAGTGGTCATGTCCTAAACATGTCCTTAC 77
|||||
Db 625 CAGTGGTCATGTCCTAAACATGTCCTTAC 654
RESULT 9
US-09-949-016-12542/c
Sequence 12542, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US/09/949,016
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12542
LENGTH: 173787
TYPE: DNA
ORGANISM: Human
US-09-949-016-12542

Query Match 2.7%; Score 22; DB 3; Length 173787;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 783 TCTCTCTCCCTCTCCCTCTCC 804
Db 113387 TCTCTCTCCCTCTCCCTCTCC 113366

RESULT 10
US-09-949-016-17302/c
Sequence 17302, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17302
LENGTH: 173791
TYPE: DNA
ORGANISM: Human
US-09-949-016-17302

Query Match 2.7%; Score 22; DB 3; Length 173791;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 783 TCTCTCTCCCTCTCCCTCTCC 804
Db 113387 TCTCTCTCCCTCTCCCTCTCC 113366

RESULT 11
US-09-949-016-53357/c
Sequence 53357, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53357
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-53357

CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 53357
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-53357

Query Match 2.6%; Score 21; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 784 CTCTCTCCCTCTCCCTCTCC 804
Db 442 CTCTCTCCCTCTCCCTCTCC 422

RESULT 12
US-09-949-016-15354/c
Sequence 15354, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15354
LENGTH: 37385
TYPE: DNA
ORGANISM: Human
US-09-949-016-15354

Query Match 2.6%; Score 21; DB 3; Length 37385;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 784 CTCTCTCCCTCTCCCTCTCC 804
Db 9330 CTCTCTCCCTCTCCCTCTCC 9310

RESULT 13
US-09-949-016-13139/c
Sequence 13139, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13139
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-13139

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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13139
; LENGTH: 95648
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)...(95648)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13139

Query Match      2.6%; Score 21; DB 3; Length 95648;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 784 CTCCTCTCCCTCTCCCTCTCC 804
Db 64354 CTCCTCTCCCTCTCCCTCTCC 64334

RESULT 14
US-09-949-016-13025/c
; Sequence 13025, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13025
; LENGTH: 102053
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(102053)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13025

Query Match      2.6%; Score 21; DB 3; Length 102053;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 784 CTCCTCTCCCTCTCCCTCTCC 804
Db 88871 CTCCTCTCCCTCTCCCTCTCC 88851

RESULT 15
US-09-949-016-15824/c
; Sequence 15824, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15824
; LENGTH: 133613
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)...(133613)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15824

Query Match      2.6%; Score 21; DB 3; Length 133613;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 784 CTCCTCTCCCTCTCCCTCTCC 804
Db 109203 CTCCTCTCCCTCTCCCTCTCC 109183

Search completed: March 5, 2006, 08:37:01
Job time : 880 secs

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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15824
; LENGTH: 133613
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)...(133613)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15824

Query Match      2.6%; Score 21; DB 3; Length 95648;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 784 CTCCTCTCCCTCTCCCTCTCC 804
Db 64354 CTCCTCTCCCTCTCCCTCTCC 64334

RESULT 14
US-09-949-016-13025/c
; Sequence 13025, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13025
; LENGTH: 102053
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(102053)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13025

Query Match      2.6%; Score 21; DB 3; Length 102053;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 784 CTCCTCTCCCTCTCCCTCTCC 804
Db 88871 CTCCTCTCCCTCTCCCTCTCC 88851

RESULT 15
US-09-949-016-15824/c
; Sequence 15824, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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sequence. The promoter sequences confer enhanced expression of operably linked genes in monocot or dicot male reproductive tissues, such as anthers, especially wheat anthers and is useful for regulating transcription of a DNA sequence, by operably linking the DNA sequence to the promoter. The promoter sequences are useful in plants to regulate the promoter. The promoter sequences are useful for control of fertility, transcription of target genes including genes for control of fertility, insect or pathogen tolerance and herbicide tolerance. They are also useful as probes or primers in nucleic acid hybridisation experiments. The promoter sequences can be used in hybridisation assays of other plant tissues to identify closely related or homologous genes and associated regulatory sequences. AAS96558-AAS96577 represent the corn promoter sequences of the present invention

XX Sequence 823 BP; 244 A; 209 C; 161 G; 209 T; 0 U; 0 Other;

Query Match 100.0%; Score 823; DB 6; Length 823;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACGGTACTCCAAAGTATAGACACAGCTAAACACACATATGCGTGGTCAATC 60
DB |||||
QY 1 CTGACGGTACTCCAAAGTATAGACACAGCTAAACACACATATGCGTGGTCAATC 60
DB |||||
QY 61 TAAACATGCTGTACCAATATTCATTGTATCAATCAGAACATTCATTAATTAAGTGA 120
DB |||||
QY 61 TAAACATGCTGTACCAATATTCATTGTATCAATCAGAACATTCATTAATTAAGTGA 120
DB |||||
QY 121 CCAATCAGATAGTCTCTCTCCGAAATATAGAGCTAAGACACTGTCTTCGTCAGATA 180
DB |||||
QY 121 CCAATCAGATAGTCTCTCTCCGAAATATAGAGCTAAGACACTGTCTTCGTCAGATA 180
DB |||||
QY 181 CATGCTTGAGATTTTTCATTCACCCCTAGACACACTCTAAGACACACTTTAAGAC 240
DB |||||
QY 181 CATGCTTGAGATTTTTCATTCACCCCTAGACACACTCTAAGACACACTTTAAGAC 240
DB |||||
QY 241 ACCCATGTCATGCTTCACTGAGCTGAGCTAGTGGGCTTCAAGAACCAACCATG 300
DB |||||
QY 241 ACCCATGTCATGCTTCACTGAGCTGAGCTAGTGGGCTTCAAGAACCAACCATG 300
DB |||||
QY 301 TACAGTTGTTCAACGCTGAATGTTTATTTGCTTCAGATTTAAAGCTAATTTAGACTGA 360
DB |||||
QY 301 TACAGTTGTTCAACGCTGAATGTTTATTTGCTTCAGATTTAAAGCTAATTTAGACTGA 360
DB |||||
QY 361 TGCAGCTGCAATTCATAGACACAAAACAGTGTAGAGCCGTATAGCATTAAGCAACA 420
DB |||||
QY 361 TGCAGCTGCAATTCATAGACACAAAACAGTGTAGAGCCGTATAGCATTAAGCAACA 420
DB |||||
QY 421 AGCGACATTTGCTAGCTACACCAATTTGCTGGGCTTCCATGGGCTCGCAGAAAGTATT 480
DB |||||
QY 421 AGCGACATTTGCTAGCTACACCAATTTGCTGGGCTTCCATGGGCTCGCAGAAAGTATT 480
DB |||||
QY 481 GTGGCTGCATATTTGCTGAAATTTATAGCGAGGCCCAAGGCCCATCTTCACTTCGAGT 540
DB |||||
QY 481 GTGGCTGCATATTTGCTGAAATTTATAGCGAGGCCCAAGGCCCATCTTCACTTCGAGT 540
DB |||||
QY 541 CAGCATTTGCTTTTAAAGCTTCGATAAATTTGCTTCACTTAAATAGACAGCTCAA 600
DB |||||
QY 541 CAGCATTTGCTTTTAAAGCTTCGATAAATTTGCTTCACTTAAATAGACAGCTCAA 600
DB |||||
QY 601 TTCTGCTTCTAGTCAACATGCTTGGATCCACGGGGGAGGAGGAGACGATGTGGGCC 660
DB |||||
QY 601 TTCTGCTTCTAGTCAACATGCTTGGATCCACGGGGGAGGAGGAGACGATGTGGGCC 660
DB |||||
QY 661 GCGCAGTGGAGCCAGCCGAGCCGCTGCTCGTCCAAACCCCTCGTTTACTAT 720
DB |||||
QY 661 GCGCAGTGGAGCCAGCCGAGCCGCTGCTCGTCCAAACCCCTCGTTTACTAT 720
DB |||||
QY 721 ATATACACAGCCAGTACCATTCATTCGTTGCTAGAGCACTGAAACAGCCGAGC 780
DB |||||
QY 721 ATATACACAGCCAGTACCATTCATTCGTTGCTAGAGCACTGAAACAGCCGAGC 780
DB |||||
QY 781 GATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGCAG 823
DB |||||

DB 781 GATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGCAG 823

RESULT 2

AAS96566

ID AAS96566 standard; DNA; 1587 BP.

XX AAS96566;

AC AAS96566;

DT 26-FEB-2002 (first entry)

XX Corn promoter sequence #9.

DE

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Novel promoters isolated from corn for controlling gene expression in male reproductive tissues, such as anthers, tassels, and to regulate transcription of target genes including genes for insect or pathogen tolerance.

Claim 1; Page 111-112; 121pp; English.

The present invention relates to the isolation of plant regulatory sequences from the male reproductive tissues of corn (Zea mays). The promoter sequences, fragments, regions or cis elements of the sequences, are capable of regulating transcription of an operably linked DNA sequence. The promoter sequences confer enhanced expression of operably linked genes in monocot or dicot male reproductive tissues, such as anthers, especially wheat anthers and is useful for regulating transcription of a DNA sequence, by operably linking the DNA sequence to the promoter. The promoter sequences are useful in plants to regulate the promoter. The promoter sequences are useful for control of fertility, insect or pathogen tolerance and herbicide tolerance. They are also useful as probes or primers in nucleic acid hybridisation experiments. The promoter sequences can be used in hybridisation assays of other plant tissues to identify closely related or homologous genes and associated regulatory sequences. AAS96558-AAS96577 represent the corn promoter sequences of the present invention

Sequence 1587 BP; 435 A; 385 C; 375 G; 392 T; 0 U; 0 Other;

Query Match 57.5%; Score 473; DB 6; Length 1587;
Best Local Similarity 100.0%; Pred. No. 4.9e-240;
Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 351 TTAGACTGATGCGAGCTGCAATTTATAGACACAAAACAGTGTAGAGCCGTATAGCAT 410
DB |||||
QY 411 TAAGCAACACAGCAACATTTCTAGCTACACCAATTTGCTGGCTTCATGGGCATCG 470
DB |||||
QY 1151 TAAGCAACACAGCAACATTTCTAGCTACACCAATTTGCTGGCTTCATGGGCATCG 1210
QY 471 CAGAGTATTGCTGCTGATATTGCTGAATTTATAGCGAGGCCCAAGGCCCATCTTC 530

Db	1211	CAGAAGTATTGTGGCTGCATATTGCTGAAATTATAGGAGGGCCCAAGGCCCATCACTTC	1270	PR	18-MAY-1999;	99US-0134768P.
Qy	531	ACTTCGAGGTGAGCATTTGTTTGTAAAGTCTCGATAAATTTGTTTCACTTAAATAG	590	PR	19-MAY-1999;	99US-0134941P.
Db	1271	ACTTCGAGGTGAGCATTTGTTTGTAAAGTCTCGATAAATTTGTTTCACTTAAATAG	1330	PR	21-MAY-1999;	99US-0135124P.
Qy	591	ACCAAGTTCAATTTCTGGTTCTAGTCAACATGCTGGATCCACGGGGGAGCGAGAGCGAA	650	PR	24-MAY-1999;	99US-0135353P.
Db	1331	ACCAAGTTCAATTTCTGGTTCTAGTCAACATGCTGGATCCACGGGGGAGCGAGAGCGAA	1390	PR	25-MAY-1999;	99US-0135629P.
Qy	651	TGTGTGCCCGCCGACGTGAGGCCAAGCCGAGCCCGGTCTCGTCCATCCAAACCCCCCTCG	710	PR	27-MAY-1999;	99US-0136021P.
Db	1391	TGTGTGCCCGCCGACGTGAGGCCAAGCCGAGCCCGGTCTCGTCCATCCAAACCCCCCTCG	1450	PR	01-JUN-1999;	99US-0136392P.
Qy	711	TTTATATATATATATACACAGACGACATACCCATATCGTGGTCTAGAGCAACTGAAA	770	PR	03-JUN-1999;	99US-0136782P.
Db	1451	TTTATATATATATATACACAGACGACATACCCATATCGTGGTCTAGAGCAACTGAAA	1510	PR	04-JUN-1999;	99US-0137222P.
Qy	771	ACAGCGAGCGATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGCAG	823	PR	07-JUN-1999;	99US-0137502P.
Db	1511	ACAGCGAGCGATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGCAG	1563	PR	08-JUN-1999;	99US-0137724P.
RESULT 3						
AAC43750						
ID	AAC43750 standard; DNA; 769 BP.					
XX	AAC43750;					
DT	18-OCT-2000 (first entry)					
DE	Zea mays DNA fragment SEQ ID NO: 40373.					
KW	Hybridisation assay; genetic mapping; gene expression control;					
KW	protein identification; signal transduction pathway; metabolic; pathway;					
KW	promoter; termination sequence; corn; ss.					
OS	Zea mays subsp. mays.					
PN	EP1033405-A2.					
XX	06-SEP-2000.					
PD	25-FEB-2000; 2000EP-00301439.					
PF	25-FEB-1999; 99US-0121825P.					
PR	05-MAR-1999; 99US-0123180P.					
PR	09-MAR-1999; 99US-0123548P.					
PR	23-MAR-1999; 99US-0125788P.					
PR	25-MAR-1999; 99US-0126264P.					
PR	29-MAR-1999; 99US-0126785P.					
PR	01-APR-1999; 99US-0127462P.					
PR	06-APR-1999; 99US-0128234P.					
PR	08-APR-1999; 99US-0128714P.					
PR	16-APR-1999; 99US-0129845P.					
PR	19-APR-1999; 99US-0130077P.					
PR	21-APR-1999; 99US-0130449P.					
PR	23-APR-1999; 99US-0130510P.					
PR	28-APR-1999; 99US-0130891P.					
PR	30-APR-1999; 99US-0131449P.					
PR	30-APR-1999; 99US-0132048P.					
PR	04-MAY-1999; 99US-0132407P.					
PR	04-MAY-1999; 99US-0132484P.					
PR	05-MAY-1999; 99US-0132485P.					
PR	06-MAY-1999; 99US-0132486P.					
PR	06-MAY-1999; 99US-0132487P.					
PR	07-MAY-1999; 99US-0132863P.					
PR	11-MAY-1999; 99US-0134207P.					
PR	14-MAY-1999; 99US-0134218P.					
PR	14-MAY-1999; 99US-0134219P.					
PR	14-MAY-1999; 99US-0134221P.					
PR	14-MAY-1999; 99US-0134370P.					

PR 27-JUL-1999; 99US-0145913P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147030P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148313P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149428P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.

Query Match 9.0%; Score 74; DB 3; Length 769;
Best Local Similarity 100.0%; Pred. No. 2.4e-28; Indels 0; Gaps 0;
Matches 74; Conservative 0; Mismatches 0;

QY 749 GTGGTGCTAGAAACCAACTGAAAAACAGCGCAGCATCTCTTCCCTCTCCCTCTCCGATC 808
Db 1 GTGGTGCTAGAAACCAACTGAAAAACAGCGCAGCATCTCTTCCCTCTCCCTCTCCGATC 60

QY 809 CATTCTCCAGCGCA 822
Db 61 CATTCTCCAGCGCA 74

RESULT 4
ADX49209/c
ID ADX49209 standard; cDNA; 485 BP.
XX
AC ADX49209;
XX
DT 21-APR-2005 (first entry)
XX
DE Plant full length insert polynucleotide seqid 23949.
XX
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
protein content; Gene; ss.
XX
OS Unidentified.
XX
PN US2004034888-A1.
XX
PD 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIU/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAO/) CAO Y.
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
DR New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX
PS Claim 1; SEQ ID NO 23949; 15pp; English.
XX
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US Patent office at
CC ftp.seqdata.uspto.gov/sequence.html?DocId:2004034888. The polynucleotide

CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX SQ Sequence 485 BP; 120 A; 126 C; 129 G; 110 T; 0 U; 0 Other;

Query Match 7.7%; Score 63; DB 13; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TGTCTTGAGATTTTATCATTCACCCCTAGACACACTTAAGACACAACCTTAAGACAC 242
DB 362 TGTCTTGAGATTTTATCATTCACCCCTAGACACACTTAAGACACAACCTTAAGACAC 303

QY 243 CCA 245
DB 302 CCA 300

RESULT 5
ADX33652
ID ADX33652 standard; cDNA; 821 BP.
XX AC ADX33652;
XX DT 21-APR-2005 (first entry)
XX DE Plant full length insert polynucleotide seqid 16472.
XX KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX OS Unidentified.
XX PN US2004034888-A1.
XX PD 19-FEB-2004.
XX PP 28-APR-2003; 2003US-00425114.
XX PR 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCREEN/) SCREEN S E.
PA (TABAKA/) TABASKA J E.
PA (CAOV/) CAO Y.
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX DR New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT

PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX PS Claim 1; SEQ ID NO 16472; 15pp; English.
XX CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX SQ Sequence 821 BP; 187 A; 227 C; 214 G; 193 T; 0 U; 0 Other;

Query Match 7.5%; Score 62; DB 13; Length 821;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 762 CAACTGAAAACAGCCGAGCGATCTCTCTCCCTCTCCCTCTCCGATCCATTCTCCAGCGC 821
DB 1 CAACTGAAAACAGCCGAGCGATCTCTCTCCCTCTCCCTCTCCGATCCATTCTCCAGCGC 60

QY 822 AG 823
DB 61 AG 62

RESULT 6
ADX30094
ID ADX30094 standard; cDNA; 791 BP.
XX AC ADX30094;
XX DT 21-APR-2005 (first entry)
XX DE Plant full length insert polynucleotide seqid 12914.
XX KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX OS Unidentified.
XX PN US2004034888-A1.
XX PD 19-FEB-2004.
XX PP 28-APR-2003; 2003US-00425114.
XX PR 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCREEN/) SCREEN S E.

PA (TABAKA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX Claim 1; SEQ ID NO 12914; 15pp; English.
 XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 XX Sequence 791 BP; 181 A; 215 C; 215 G; 180 T; 0 U; 0 Other;
 SQ Query Match 7.2%; Score 59; DB 13; Length 791;
 Best Local Similarity 100.0%; Pred. No. 2.2e-20;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 765 CTGAAACAGCCGAGCGATCTCTCTCCCTCTCCGATCCATTCTCCAGGCGAG 823
 DB 1 CTGAAACAGCCGAGCGATCTCTCTCCCTCTCCGATCCATTCTCCAGGCGAG 59
 RESULT 7
 ID ADX30071 standard; cDNA; 795 BP.
 XX ADX30071;
 XX 21-APR-2005 (first entry)
 XX Plant full length insert polynucleotide seqid 12891.
 DE plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.
 OS Unidentified.
 XX US2004034888-A1.
 XX 19-FEB-2004.
 XX 28-APR-2003; 2003US-00425114.
 XX 06-MAY-1999; 99US-00304517.
 XX 05-NOV-2001; 2001US-00985678.

XX (LIUJ/) LIU J.
 PA (ZHOU/) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAKA/) TABASKA J E.
 PA (CAOY/) CAO Y.
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 PI WPI; 2004-180133/17.
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX Claim 1; SEQ ID NO 12891; 15pp; English.
 XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for increasing the rate of homologous
 CC lignin or plant growth regulators, for improving yield by modification of
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 XX Sequence 795 BP; 181 A; 215 C; 215 G; 184 T; 0 U; 0 Other;
 SQ Query Match 7.2%; Score 59; DB 13; Length 795;
 Best Local Similarity 100.0%; Pred. No. 2.2e-20;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 765 CTGAAACAGCCGAGCGATCTCTCTCCCTCTCCGATCCATTCTCCAGGCGAG 823
 DB 1 CTGAAACAGCCGAGCGATCTCTCTCCCTCTCCGATCCATTCTCCAGGCGAG 59
 RESULT 8
 ID ADX33856 standard; cDNA; 781 BP.
 XX ADX33856;
 XX 21-APR-2005 (first entry)
 XX Plant full length insert polynucleotide seqid 16676.
 DE plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.
 OS Unidentified.
 XX US2004034888-A1.
 XX 19-FEB-2004.

XX PF 28-APR-2003; 2003US-00425114.
XX PR 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX (LIUJ/) LIU J.
XX PA (ZHOU/) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.
XX PA (TABAS/) TABASKA J E.
XX PA (CAOY/) CAO Y.
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX PT New recombinant DNA construct, useful for improving plant tolerance to
XX PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX PT pests, for conferring increased resistance to plant disease, or for
XX PT improving yield.
XX
XX PS Claim 1; SEQ ID NO 16676; 15pp; English.
XX
XX CC The invention describes a recombinant DNA construct comprising a
XX CC polynucleotide consisting of a sequence encoding an amino acid sequence
XX CC available in electronic form from the US patent office at
XX CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX CC of the invention are also useful in physical arrays of molecules and as
XX CC plant breeding markers. The recombinant DNA construct is useful for
XX CC improving plant tolerance to cold, heat, drought, herbicides, extreme
XX CC osmotic conditions, pathogens or pests, for manipulating growth rate in
XX CC plant cells by modification of the cell cycle pathway, for conferring
XX CC increased resistance to plant disease, for producing galactomannan,
XX CC lignin or plant growth regulators, for increasing the rate of homologous
XX CC recombination in plants, for improving yield by modification of
XX CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX CC or by providing improved plant growth and development under at least one
XX CC stress condition or for modifying seed oil or protein yield and/or
XX CC content. This sequence represents a plant full length insert
XX CC polynucleotide that can be used in the recombinant DNA construct of the
XX CC invention.
XX
XX SQ Sequence 781 BP; 175 A; 216 C; 209 G; 181 T; 0 U; 0 Other;
Query Match 6.0%; Score 49; DB 13; Length 781;
Best Local Similarity 100.0%; Pred. No. 4.5e-15;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 775 CCGAGCGATCTCCCTCTCCCTCTCCCTCTCCGATCCATTCCTCCAGCGCAG 823
DB 1 CCGAGCGATCTCCCTCTCCCTCTCCCTCTCCGATCCATTCCTCCAGCGCAG 49
RESULT 9
ABL76691
ID ABL76691 standard; cDNA; 307 BP.
XX
XX AC ABL76691;
XX
XX DT 14-MAY-2002 (first entry)
XX
XX DE Corn tassel-derived polynucleotide (cdps) SEQ ID NO:6065.
XX
XX KW Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPS;
XX KW inheritance; characteristic; growth; development; disease resistance;
XX KW environmental adaptability; quality; yield; molecular marker;
XX KW multigene trait; plant breeding; corn tassel; gene; ss.
XX
XX OS Zea mays.
XX
XX PN US2001051335-A1.
XX

PD XX 13-DEC-2001.
XX PF 16-APR-1999; 99US-00294093.
XX PR 21-APR-1998; 98US-0082567P.
XX (LALG/) LALGUDI R V.
XX PA (ITOL/) ITO L Y.
XX PA (SHER/) SHERMAN B K.
XX
XX PI Lalgudi RV, Ito LY, Sherman BK;
XX WPI; 2002-163647/21.
XX
XX PT Novel purified corn tassel-derived polynucleotide useful for determining
XX PT altered gene expression, to recover regulatory elements and to follow
XX PT inheritance of desirable characteristics through hybrid breeding
XX PT programs.
XX PS Claim 1; SEQ ID NO 6065; 201pp; English.
XX
XX CC The present sequence describes a purified corn tassel-derived
XX CC polynucleotide sequence (cdps) comprising a nucleic acid sequence
XX CC selected from those given in ABL70627 to ABL76833. The cdps sequences
XX CC encode corn tassel-derived polypeptides (CDPS). The cdps sequences (I)
XX CC can be used for determining altered gene expression, to recover
XX CC regulatory elements and to follow inheritance of desirable
XX CC characteristics through hybrid breeding programs. (I) are also useful in
XX CC the evaluation, and alteration of desired characteristics associated with
XX CC growth and development, disease resistance, environmental adaptability,
XX CC quality and yield, and as molecular markers for studying inheritance of
XX CC multigene traits in a plant breeding program. (I) can be used to produce
XX CC a tassel-specific profile of gene transcription, a transcript image, to
XX CC clone regulatory elements for use in transformation vectors, to express a
XX CC polypeptide, to identify, isolate or extend identical or related corn
XX CC tassel nucleic acid sequences from DNA libraries, in nucleic acid
XX CC hybridisation or amplification technologies, as query sequences to
XX CC determine homology of known sequences, as probe for use in Southern or
XX CC Northern hybridisation, and to identify the presence of and/or to
XX CC determine the degree of similarity between two (or more) nucleic acid
XX CC sequences
XX
XX SQ Sequence 307 BP; 63 A; 99 C; 81 G; 50 T; 0 U; 14 Other;
Query Match 4.9%; Score 40; DB 6; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 784 CTCCTCTCCCTCTCCCTCTCCGATCCATTCCTCCAGCGCAG 823
DB 1 CTCCTCTCCCTCTCCCTCTCCGATCCATTCCTCCAGCGCAG 40
RESULT 10
ADX60974
ID ADX60974 standard; cDNA; 1326 BP.
XX
XX AC ADX60974;
XX
XX DT 21-APR-2005 (first entry)
XX
XX DE Plant full length insert polynucleotide seqid 31817.
XX
XX KW plant protectant; plant growth regulant; gene therapy; plant;
XX KW recombinant DNA construct; physical array; plant breeding marker;
XX KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX KW extreme osmotic condition; pathogen tolerance; pest tolerance;
XX KW growth rate; cell cycle pathway; disease resistance;
XX KW galactomannan production; lignin production; plant growth regulator;
XX KW yield; plant growth; plant development; seed oil; protein yield;
XX KW protein content; gene; ss.
XX
XX OS Unidentified.

XX PN US2004034888-A1.
XX PD 19-FEB-2004.
XX PF 28-APR-2003; 2003US-00425114.
XX PR 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX PA (LIUJ/) LIU J.
XX PA (ZHOU/) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.
XX PA (TABAS/) TABASKA J E.
XX PA (CAOY/) CAO Y.
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX DR WPI; 2004-180133/17.
XX PS New recombinant DNA construct, useful for improving plant tolerance to
XX PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX PT pests, for conferring increased resistance to plant disease, or for
XX PT improving yield.
XX PS Claim 1; SEQ ID NO 31817; 15pp; English.
XX CC The invention describes a recombinant DNA construct comprising a
XX CC polynucleotide consisting of a sequence encoding an amino acid sequence
XX CC available in electronic form from the US patent office at
XX CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX CC of the invention are also useful in physical arrays of molecules and as
XX CC plant breeding markers. The recombinant DNA construct is useful for
XX CC improving plant tolerance to cold, heat, drought, herbicides, extreme
XX CC osmotic conditions, pathogens or pests, for manipulating growth rate in
XX CC plant cells by modification of the cell cycle pathway, for conferring
XX CC increased resistance to plant disease, for producing galactomannan,
XX CC lignin or plant growth regulators, for increasing the rate of homologous
XX CC recombination in plants, for improving yield by modification of
XX CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX CC or by providing improved plant growth and development under at least one
XX CC stress condition or for modifying seed oil or protein yield and/or
XX CC content. This sequence represents a plant full length insert
XX CC polynucleotide that can be used in the recombinant DNA construct of the
XX CC invention.
XX SQ Sequence 1326 BP; 353 A; 297 C; 299 G; 377 T; 0 U; 0 Other;
Query Match 4.9%; Score 40; DB 13; Length 1326;
Best Local Similarity 100.0%; Pred. No. 2.7e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 48 CAGTGTCTATGCTTAAACATGCTGTCTTACCATATTCATT 87
Db 181 CAGTGTCTATGCTTAAACATGCTGTCTTACCATATTCATT 220
RESULT 11
ADX33827
ID ADX33827 standard; cDNA; 782 BP.
XX AC ADX33827;
XX DT 21-APR-2005 (first entry)
XX DE Plant full length insert polynucleotide seqid 16647.
XX KW plant protectant; plant growth regulator; gene therapy; plant;
XX KW recombinant DNA construct; physical array; plant breeding marker;
XX KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX KW extreme osmotic condition; pathogen tolerance; pest tolerance;
XX KW growth rate; cell cycle pathway; disease resistance;

KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
XX OS Unidentified.
XX PN US2004034888-A1.
XX PD 19-FEB-2004.
XX PF 28-APR-2003; 2003US-00425114.
XX PR 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX PA (LIUJ/) LIU J.
XX PA (ZHOU/) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.
XX PA (TABAS/) TABASKA J E.
XX PA (CAOY/) CAO Y.
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX DR WPI; 2004-180133/17.
XX PS New recombinant DNA construct, useful for improving plant tolerance to
XX PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX PT pests, for conferring increased resistance to plant disease, or for
XX PT improving yield.
XX PS Claim 1; SEQ ID NO 16647; 15pp; English.
XX CC The invention describes a recombinant DNA construct comprising a
XX CC polynucleotide consisting of a sequence encoding an amino acid sequence
XX CC available in electronic form from the US patent office at
XX CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX CC of the invention are also useful in physical arrays of molecules and as
XX CC plant breeding markers. The recombinant DNA construct is useful for
XX CC improving plant tolerance to cold, heat, drought, herbicides, extreme
XX CC osmotic conditions, pathogens or pests, for manipulating growth rate in
XX CC plant cells by modification of the cell cycle pathway, for conferring
XX CC increased resistance to plant disease, for producing galactomannan,
XX CC lignin or plant growth regulators, for increasing the rate of homologous
XX CC recombination in plants, for improving yield by modification of
XX CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX CC or by providing improved plant growth and development under at least one
XX CC stress condition or for modifying seed oil or protein yield and/or
XX CC content. This sequence represents a plant full length insert
XX CC polynucleotide that can be used in the recombinant DNA construct of the
XX CC invention.
XX SQ Sequence 782 BP; 177 A; 214 C; 207 G; 184 T; 0 U; 0 Other;
Query Match 4.4%; Score 36; DB 13; Length 782;
Best Local Similarity 100.0%; Pred. No. 3.5e-08;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 788 TCTCCCTCTCCCTCTCCGATCCATTCCTCCAGGCGAG 823
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RESULT 12
ADX48086/c
ID ADX48086 standard; cDNA; 1578 BP.
XX AC ADX48086;
XX DT 21-APR-2005 (first entry)
XX DE Plant full length insert polynucleotide seqid 22826.
XX KW

KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.
 XX Unidentified.
 OS
 XX
 PN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 XX
 PF 28-APR-2003; 2003US-00425114.
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 PR 06-MAY-1999; 99US-00304517.
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 PA (LIUJ/) LIU J.
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 XX
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 PI WPI; 2004-180133/17.
 DR
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 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 PT
 XX
 PS Claim 1; SEQ ID NO 22826; 15pp; English.
 XX
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 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
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 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 SQ Sequence 1578 BP; 380 A; 391 C; 429 G; 378 T; 0 U; 0 Other;
 Query Match 4.4%; Score 36; DB 13; Length 1578;
 Best Local Similarity 100.0%; Pred. No. 3.6e-08;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 148 ATAGAGCTAAGACACTGTGCTTCGTCAGATACAT 183
 DB 908 ATAGAGCTAAGACACTGTGCTTCGTCAGATACAT 873
 RESULT 13
 AAA57891
 ID AAA57891 standard; DNA; 6343 BP.
 XX
 AC AAA57891;

XX 10-OCT-2000 (first entry)
 DT
 XX
 DE Maize glossy2 (gl2) gene.
 XX
 KW Maize; glossy2; gl2; cuticle; cuticular lipid biosynthesis;
 KW lipid composition; lipid quantity; disease resistance; pest resistance;
 KW wind resistance; frost resistance; UV resistance; transgenic plant;
 KW antisense inhibition; ds.
 XX
 OS Zea mays.
 XX
 PN US6060644-A.
 XX
 PD 09-MAY-2000.
 XX
 PF 29-DEC-1995; 95US-00581148.
 XX
 PR 24-MAR-1994; 94US-00218028.
 XX
 PA (IOWA) UNIV IOWA STATE RES FOUND INC.
 XX
 PI Schnable PS, Nikolau BJ, Xu X, Xia Y, Robertson DS, Hansen JD;
 XX WPI; 2000-349707/30.
 DR
 XX
 XX Transforming plants such as maize and canola, for producing new plant
 PT varieties having disease and pest resistance involves introducing
 PT cuticular lipid genes into the plant genome.
 PT
 XX
 PS Example 7; Col 115-122; 69pp; English.
 XX
 CC The invention relates to transforming a plant cell with either a nucleic
 CC acid encoding a plant cuticular lipid biosynthetic protein, or an
 CC antisense nucleic acid sequence targeted to a plant cuticular lipid
 CC gene, and then generating a plant from the plant cell. The cuticular
 CC lipid genes that may be used in the invention are given in AAA57871-
 CC A57884 and AAA57891. The cuticle consists of a meshwork (cutin) of cross-
 CC esterified polymerised hydroxy-fatty acids embedded in a complex mixture
 CC of nonpolar lipids (the cuticular wax). The cuticle protects and
 CC strengthens the plants, prevents evaporation of internal fluids and
 CC filters UV radiation. Mutations in the cuticular lipid genes affects the
 CC quantity and composition of cuticular lipids; in maize, 17 loci (the
 CC glossy (gl) genes) have been identified as being involved in cuticular
 CC lipid biosynthesis or control. The method is useful for introducing a
 CC nucleic acid into a cell preferably of maize, soybean, rapeseed, canola,
 CC cotton, safflower, peanut, palm or sunflower plant and generating a plant
 CC from the plant cell. The transformed plants have improved environmental
 CC resistance relating to wind, frost, UV or drought; fungal, bacterial or
 CC viral disease resistance; pest resistance; and altered lipid content in
 CC seeds. The present sequence represents the maize glossy2 (gl2) gene
 XX
 SQ Sequence 6343 BP; 1493 A; 1667 C; 1607 G; 1564 T; 0 U; 12 Other;
 Query Match 4.4%; Score 36; DB 3; Length 6343;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 101 CATTCAATAAATAAGTGACCAATCAGATAGTCTC 136
 DB 3715 CATTCAATAAATAAGTGACCAATCAGATAGTCTC 3750
 RESULT 14
 AAV63717
 ID AAV63717 standard; DNA; 6550 BP.
 XX
 AC AAV63717;
 XX
 DT 12-APR-1999 (first entry)
 XX
 DE Maize per5 root preferential cationic peroxidase gene.
 XX

KW Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root;
 KW vector; plasmid PerGUS16; beta-glucuronidase; uidA; reporter gene; ds;
 KW circular; cyclic.

OS Escherichia coli.

OS Zea mays.

OS Agrobacterium tumefaciens.

OS Synthetic.

OS Chimeric.

XX

FH Key Location/Qualifiers
 FT promoter 48..4247
 FT /tag= a
 FT /note= "per5 promoter and untranslated leader"
 FT exon 4248..4263
 FT /tag= b
 FT /note= "per5 exon 1"
 FT CDS 4264..6068
 FT /tag= c
 FT /product= "beta-glucuronidase"
 FT /note= "Escherichia coli uidA reporter gene"
 FT 3'UTR 6069..6111
 FT /tag= d
 FT /note= "3' untranslated region from pBI221"
 FT 3'UTR 6122..6396
 FT /tag= e
 FT /note= "nos 3'UTR"
 FT misc_feature 6397..6407
 FT /tag= f
 FT /note= "linker"
 FT misc_feature 6408..9299
 FT /tag= g
 FT /note= "Bluescript II SK-"

XX WO9856921-A1.

PN

XX

XX

PD 17-DEC-1998.

XX 10-JUN-1998; 98WO-US011921.

PF

XX 12-JUN-1997; 97US-0049752P.

PR

XX (DOWC) DOW AGROSCIENCES LLC.

PA

XX Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA;

PI Pareddy D, Petolino JF, Smith K, Woosley A;

PI

XX WPI; 1999-080904/07.

DR

XX New isolated regulatory sequences for transgenic plants - which are

PT derived from the maize root preferential cationic peroxidase protein

FT (per5) gene.

FT

XX Example 11; Page 108-112; 150pp; English.

PS

XX This is the nucleotide sequence of PerGUS, a plasmid containing 4 kb of

CC the maize root preferential cationic peroxidase per5 gene comprising the

CC per5 promoter, untranslated leader, and the first 5 codons of the coding

CC region (i.e. nucleotides 1-4200 of the sequence given in AAV63717), as

CC well as the GUS gene, and the nos 3' untranslated region (3'UTR). It does

CC not include an intron in the untranslated region. The invention relates

CC to new isolated regulatory sequences, especially promoter, intron and

CC 3'UTR sequences, of the maize per5 gene. Claimed recombinant gene

CC cassettes comprising per5 regulatory sequences are used to control

CC expression of recombinant genes in selected tissue, especially the root,

CC of transformed plants, particularly maize

XX

SQ Sequence 9299 BP; 2573 A; 2114 C; 2158 G; 2453 T; 0 U; 1 Other;

Query Match

Best Local Similarity 3.9%; Score 32; DB 2; Length 9299;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 TCTAAACATGTCCTTACCATATTCATTGTA 90
 DB 1462 TCTAAACATGTCCTTACCATATTCATTGTA 1493

Search completed: March 5, 2006, 11:35:52
 Job time : 560 secs

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Best Local Similarity 100.0%; Pred. No. 4.9e-10; Length 198102;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 CAATCAGAACATTCATTAATTAAGTGACCAATCAG 128
Db 173568 CAATCAGAACATTCATTAATTAAGTGACCAATCAG 173604

/estimated_length=100

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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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X88779.1 GI:949979
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1
REFERENCE
AUTHORS
Tacke, E., Korfhaage, C., Michel, D., Maddaloni, M., Motto, M.,
Lanzini, S., Salamini, F. and Döring, H.P.
Transposon tagging of the maize Glossy2 locus with the transposable
element En/Spm
Plant J. 8 (6), 907-917 (1995).
2 (bases 1 to 6343)
PUBLISHED
JOURNAL
Tacke, E.
REFERENCE
AUTHORS
Tacke, E.
TITLE
Direct Submission
Submitted (19-JUN-1995) E. Tacke, Max-Planck-Institute, Dept.
Salamini, Carl-von-Linne-Weg 10, 50829 Köln, NRW, FRG
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/notes="Glossy2 locus; G12"
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VGPTEDLWLVPAADAGMACYSFHSVSDAHLKLHQQONGRQDAAGTFLVSAALYQVA
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ETRAVAAFGQDVLVYGANLTLVDMEQVDLYGLEIKGQRPVHVEYMGVDGEGAVLV
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2608..3923
/number=1
/genes="orf"
3924..5001
/number=2

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exon
gene
CDS
intron
exon
ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-09; Length 6343;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 CATTCAATAAATTAAGTGACCAATCAGATAGTCTC 136
Db 3715 CATTCAATAAATTAAGTGACCAATCAGATAGTCTC 3750

RESULT 14
AC149816/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AC149816
Zea mays clone ZMBBB0309E13, *** SEQUENCING IN PROGRESS ***, 7
unordered pieces.
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEPIN.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 69497)
REFERENCE
AUTHORS
Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K.
and Messing, J.
Zea mays, clone ZMBBB0309E13
2 (bases 1 to 69497)
Unpublished
JOURNAL
REFERENCE
AUTHORS
Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K.,
Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,
Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S.,
Dooley, K., Dorris, L., Erickson, J., Farrow, S., Ferreira, P.,
FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L.,
Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P.,
Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 69497)
REFERENCE
AUTHORS
Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K.,
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Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (03-FEB-2005) Broad Institute of MIT and Harvard, 320
Charles Street, Cambridge, MA 02141, USA
TITLE
JOURNAL
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 PA (TAB//) TABASKA J E.
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 XX WPI; 2004-180133/17.
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 DB 908 ATAGAGCTAAGACATGCTGCTCTTCGTCAGATACAT 873
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 AC AAAS7891;

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 XX Zea mays.
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 PI Schnable PS, Nikolau BJ, Xu X, Xia Y, Robertson DS, Hansen JD;
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 DR WPI; 2000-349707/30.
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 CC The invention relates to transforming a plant cell with either a nucleic
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 CC esterified polymerised hydroxy-fatty acids embedded in a complex mixture
 CC of nonpolar lipids (the cuticular wax). The cuticle protects and
 CC strengthens the plants, prevents evaporation of internal fluids and
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 CC nucleic acid into a cell preferably of maize, soybean, rapeseed, canola,
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 CC from the plant cell. The transformed plants have improved environmental
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 CC viral disease resistance; pest resistance; and altered lipid content in
 CC seeds. The present sequence represents the maize glossy2 (gl2) gene
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 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 101 CATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 136
 DB 3715 CATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 3750
 RESULT 14
 AAAS7891
 ID AAAS7891 standard; DNA; 6550 BP.
 XX
 AC AAAS7891;
 XX
 DT 12-APR-1999 (first entry)
 XX
 DE Maize per5 root preferential cationic peroxidase gene.
 XX

KW Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root; ds.
 XX Zea mays.
 XX
 FH Key
 FT promoter
 FT Location/Qualifiers
 FT 1. .4215
 FT /tag= a
 FT /note= "this region is specifically claimed in Claim 1"
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 FT /tag= g
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 FT 4201. .6068
 FT /tag= m
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 FT /note= "contains introns"
 FT 4201. .4425
 FT /tag= n
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 FT 4420. .5064
 FT /tag= o
 FT /note= "this sequence is specifically claimed in Claim 2"
 FT 4426. .5058
 FT /tag= p
 FT /number= 1
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 FT 5059. .5250
 FT /tag= q
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 FT 5245. .5388
 FT /tag= r
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 FT 5251. .5382
 FT /tag= s
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 FT 5542. .5654
 FT /tag= u
 FT /note= "this sequence is specifically claimed in Claim 2"
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 FT /tag= x

FT intron
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 FT /number= 3
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 FT 6068. .6431
 FT /tag= y
 FT /note= "transcription termination sequence, specifically claimed in Claim 3"
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 XX
 PN WO9856921-A1.
 XX 17-DEC-1998.
 PD
 PF 10-JUN-1998; 98WO-US011921.
 XX
 PR 12-JUN-1997; 97US-0049752P.
 XX
 PA (DOWC) DOW AGROSCIENCES LLC.
 XX
 PI Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA;
 PI Pareddy D, Petolino JF, Smith K, Woosley A;
 XX
 DR WPI; 1999-080904/07.
 XX P-PSDB; AAW87893.
 XX
 PT New isolated regulatory sequences for transgenic plants - which are
 PT derived from the maize root preferential cationic peroxidase protein
 PT (per5) gene.
 XX
 PS Claim 1; Page 84-89; 150pp; English.
 XX
 CC This is the nucleotide sequence of the maize per5 root preferential
 CC cationic peroxidase gene, which encodes a 333-amino acid peroxidase
 CC polypeptide (see AAW87893). Genomic clones comprising per5 sequences were
 CC isolated from a maize W22 genomic library using a probe based on isolated
 CC per5 cDNA. Overlapping subfragments of the gene were sequenced to
 CC determine the complete 6550 bp sequence of the per5 gene. Regulatory
 CC sequences derived from the per5 gene, including the promoter, introns and
 CC 3' untranslated region (3'UTR), are used in claimed recombinant gene
 CC cassettes for controlling expression of recombinant genes in selected
 CC tissue, especially the root, of transformed plants, particularly maize.
 CC The gene cassettes can be used for expression of heterologous genes such
 CC as those that confer tolerance to herbicides, insects or viruses, and
 CC genes that provide improved nutritional value or processing
 CC characteristics to the plant. Use of the per5 3'UTR sequences provides
 CC enhanced expression compared to similar gene cassettes utilising the nos
 CC 3'UTR
 XX
 SQ Sequence 6550 BP; 1844 A; 1427 C; 1346 G; 1933 T; 0 U; 0 Other;
 Query Match 3.9%; Score 32; DB 2; Length 6550;
 Best Local Similarity 100.0%; Pred.No. 4.9e-06;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 59 TCTAAACATGCTGTACCATATTCATTGTA 90
 DB 1415 TCTAAACATGCTGTACCATATTCATTGTA 1446
 RESULT 15
 AAV63730
 ID AAV63730 standard; DNA; 9299 BP.
 XX
 AC AAV63730;
 XX
 DT 12-APR-1999 (first entry)
 XX
 DE Vector plasmid PerGUS16.
 XX

KW Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root;
KW vector; plasmid perGUS16; beta-glucuronidase; uida; reporter gene; ds;
KW circular; cyclic.

XX Escherichia coli.

OS Zea mays.

OS Agrobacterium tumefaciens.

OS Synthetic.

OS Chimeric.

XX

PH Key

FT promoter

FT 48.4247

FT /tag= a

FT /note= "per5 promoter and untranslated leader"

FT exon

FT 4248.4263

FT /tag= b

FT /note= "per5 exon 1"

FT CDS

FT 4264.6068

FT /tag= c

FT /product= "beta-glucuronidase"

FT /note= "Escherichia coli uida reporter gene"

FT 3'UTR

FT 6089.6111

FT /tag= d

FT /note= "3' untranslated region from pBI221"

FT 3'UTR

FT 6122.6396

FT /tag= e

FT /note= "nos 3'UTR"

FT misc_feature

FT 6397.6407

FT /tag= f

FT /note= "linker"

FT misc_feature

FT 6408.9299

FT /tag= g

FT /note= "Bluescript II SK"

FT

XX

PN WO9856921-A1.

XX

XX

PD 17-DEC-1998.

XX

XX 10-JUN-1998; 98WO-US011921.

XX

XX 12-JUN-1997; 97US-0049752P.

XX

XX (DWC) DOW AGROSCIENCES LLC.

XX

PI Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA;

PI Fareddy D, Petolino JF, Smith K, Woosley A;

XX

DR WPI; 1999-080904/07.

XX

XX New isolated regulatory sequences for transgenic plants - which are

PT derived from the maize root preferential cationic peroxidase protein

PT (per5) gene.

XX

XX Example 11; Page 108-112; 150pp; English.

PS

XX

This is the nucleotide sequence of PerCUS, a plasmid containing 4 kb of the maize root preferential cationic peroxidase per5 gene comprising the per5 promoter, untranslated leader, and the first 5 codons of the coding region (i.e. nucleotides 1-4200 of the sequence given in AAV63717), as well as the GUS gene, and the nos 3' untranslated region (3'UTR). It does not include an intron in the untranslated region. The invention relates to new isolated regulatory sequences, especially promoter, intron and 3'UTR sequences, of the maize per5 gene. Claimed recombinant gene cassettes comprising per5 regulatory sequences are used to control expression of recombinant genes in selected tissue, especially the root, of transformed plants, particularly maize

SQ Sequence 9299 BP; 2573 A; 2114 C; 2158 G; 2453 T; 0 U; 1 Other;

Query Match

Best Local Similarity 3.9%; Score 32; DB 2; Length 9299;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model
Run on: March 5, 2006, 11:18:36 ; Search time 4262 seconds
(without alignments)
10976.574 Million cell updates/sec

Title: US-10-660-208-90
Perfect score: 823
Sequence: 1 ctgcacggtactccaagtat.....cgatccattctccagcgacg 823

Scoring: ~~gapop 60.0, Gapext 60.0~~
Gapop 60.0, Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Words: ~~zeta~~

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	823	100.0	823	6	AX299949 Sequence
2	473	57.5	1587	6	AX299946 Sequence
3	103	12.5	149882	14	AC155395 Zea mays
4	76	9.2	182004	14	AC155608 Zea mays
5	73	8.9	110000	15	Continuation (2 of
6	61	7.4	193326	14	AC155578 Zea mays
7	50	6.1	148120	14	AC155517 Zea mays
8	46	5.6	112468	14	AC149836 Zea mays
9	46	5.6	143793	14	AC149827 Zea mays
10	40	4.9	132900	14	AC166637 Zea mays
11	38	4.6	830	15	ZMPRO2MR
12	37	4.5	198102	14	AC145389 Zea mays
13	36	4.4	6343	15	ZMGLQSSY
14	26	4.4	69497	14	AC149816 Zea mays
15	35	4.3	1257	15	AF348367 Zea mays
16	35	4.3	1437	15	ZMU29160 Zea mays
17	35	4.3	134692	14	AC151050 Zea mays
18	35	4.3	169976	15	AY883559 Zea mays

c	19	4.1	117844	14	AC155360	Zea mays
c	20	4.1	170318	14	AC155367	Zea mays
c	21	4.1	189962	14	AC148165	Zea mays
c	22	4.0	116794	14	AC149633	Zea mays
c	23	4.0	160351	14	AC148152	Zea mays
c	24	4.0	187674	14	AC149640	Zea mays
c	25	3.9	6550	6	BD132692	Regulator
c	26	3.9	6550	6	AR208995	Sequence
c	27	3.9	6550	6	AR482064	Sequence
c	28	3.9	9299	6	BD132705	Regulator
c	29	3.9	9299	6	AR209008	Sequence
c	30	3.9	9299	6	AR482077	Sequence
c	31	3.9	9408	6	BD132706	Regulator
c	32	3.9	9408	6	AR209009	Sequence
c	33	3.9	9408	6	AR482078	Sequence
c	34	3.9	181757	14	AC146713	Zea mays
c	35	3.6	720	6	AR649754	Sequence
c	36	3.6	720	6	AX406847	Sequence
c	37	3.6	133685	14	AC155399	Zea mays
c	38	3.4	164241	14	AC155575	Zea mays
c	39	3.3	63760	14	AC147518	Zea mays
c	40	3.3	119531	14	AC155407	Zea mays
c	41	3.3	147470	15	AC157776	Zea mays
c	42	3.3	175006	14	AC155579	Zea mays
c	43	3.0	38	6	AX299923	Sequence
c	44	2.9	110000	15	AP008215	Continuation (70 o
c	45	2.9	110000	15	AP008208_079	Continuation (80 o

ALIGNMENTS

RESULT 1
AX299949
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

AX299949
Sequence 90 from Patent WO0183790.
AX299949
AX299949.1 GI:17129440
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

Conner, T.W., Dubois, P., Malven, M., and Masucci, J.D.
Plant regulatory sequences for selective control of gene expression
Patent: WO 0183790-A 90 08-NOV-2001;
Monsanto Technology LLC (US)

Location/Qualifiers
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/organism="Zea mays"
/mol_type="unassigned DNA"
/db_xref="taxon:4577"

Query Match	100.0%	Score	823	DB	6	Length	823
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Matches	823	Conservative	0	Mismatches	0	Indels	0
Gap	0						
QY	1	CTGCACGGTACTCCAAGTATAGACACAGCTAAACACACATTAATGTCATGTC	60				
Db	1	CTGCACGGTACTCCAAGTATAGACACAGCTAAACACACATTAATGTCATGTC	60				
QY	61	TAACAATGTCCTTACCATTATTCATGTCATGTCATGTCATGTCATGTCATGTC	120				
Db	61	TAACAATGTCCTTACCATTATTCATGTCATGTCATGTCATGTCATGTCATGTC	120				
QY	121	CCAATCAGATAGTCCTGTCGCGAATATAGACACAGCTGTCCTTCGTCAGATA	180				
Db	121	CCAATCAGATAGTCCTGTCGCGAATATAGACACAGCTGTCCTTCGTCAGATA	180				
QY	181	CATGCTTGGAGATTTTATACATTCACCCCTTAGACACACTCTAAGACACACTTAAGAC	240				

Db	181	CATGCTTTGAGATTTT TACATTTACCCCTTAGACACACTCTTAAGACACAACACTTAAGAC	240		
Qy	241	ACCCATTGTACATGCCCTAACTGGCAGCGCTACGTAGGGGCTATTCAAGAACCAACACCATG	300		
Db	241	ACCCATTGTACATGCCCTAACTGGCAGCGCTACGTAGGGGCTATTCAAGAACCAACACCATG	300		
Qy	301	TACAGTTGTTGCAACGTAATGGTTATTGCTTCAGATTAAGCTAAATTTTAGACTGA	360		
Db	301	TACAGTTGTTGCAACGTAATGGTTATTGCTTCAGATTAAGCTAAATTTTAGACTGA	360		
Qy	361	TGCAGCTGCAATTCATAGAGACAAAACAGTGTAGAGCCGTTAAGCAATTAAGCAACA	420		
Db	361	TGCAGCTGCAATTCATAGAGACAAAACAGTGTAGAGCCGTTAAGCAATTAAGCAACA	420		
Qy	421	AGCGAACATTGCTTAGCTACAACTTTGCTGGGCTTCCATGGGCATCGCAGAAGTATT	480		
Db	421	AGCGAACATTGCTTAGCTACAACTTTGCTGGGCTTCCATGGGCATCGCAGAAGTATT	480		
Qy	481	GTGGCTGCATATTGCTGAAATTTATAGCAGGCGCCCAAGGCCCATCACTTCGAGGT	540		
Db	481	GTGGCTGCATATTGCTGAAATTTATAGCAGGCGCCCAAGGCCCATCACTTCGAGGT	540		
Qy	541	CAGCAATTCATTTGTTAAAGCTCTCGATAAATTTGTTCACTTAAATATAGACCAAGTCAA	600		
Db	541	CAGCAATTCATTTGTTAAAGCTCTCGATAAATTTGTTCACTTAAATATAGACCAAGTCAA	600		
Qy	601	TTCTGTTTCTAGTCAACATCGCTCGATCCAGGGGGAGCGAGGACGAAATGTGGGCC	660		
Db	601	TTCTGTTTCTAGTCAACATCGCTCGATCCAGGGGGAGCGAGGACGAAATGTGGGCC	660		
Qy	661	GCCGAGTGAGCCCAAGCGAGCCCGCTCGCTCCGTCCTCAACACCCCTCGTTTACTAT	720		
Db	661	GCCGAGTGAGCCCAAGCGAGCCCGCTCGCTCCGTCCTCAACACCCCTCGTTTACTAT	720		
Qy	721	ATATACACAGCGCAGCATACCATATCGTGTGCTAGAGCACTGAAACAGCCGAGC	780		
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Qy	781	GATCTCTCTCCCTCTCCCTCTCCGATCCATTTCCAGCGCAG	823		
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LOCUS	Sequence 87 from Patent WO0183790.				
DEFINITION	AX299946				
ACCESSION	AX299946				
VERSION	AX299946.1	GI:17129437			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
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Best Local Similarity	100.0%;	Pred. No. 4e-278;			
Matches 473;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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* 24623	contig of 2947 bp in length	gap	gap	/estimated_length=unknown
* 24624	24723:	gap of unknown length	gap	32649..32748
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* 28117	28216:	gap of unknown length	gap	40513..40612
* 28217	28534:	contig of 1118 bp in length	gap	/estimated_length=unknown
* 29535	29634:	gap of unknown length	gap	43862..43961
* 32649	32748:	contig of 3014 bp in length	gap	/estimated_length=unknown
* 32649	32748:	gap of unknown length	gap	48430..48529
* 40513	40612:	contig of 7764 bp in length	gap	/estimated_length=unknown
* 40613	43861:	contig of 3249 bp in length	gap	59230..59329
* 43862	43961:	gap of unknown length	gap	/estimated_length=unknown
* 43962	48429:	contig of 4468 bp in length	gap	60890..60989
* 48430	48529:	gap of unknown length	gap	/estimated_length=unknown
* 48530	59229:	contig of 10700 bp in length	gap	65148..65247
* 59230	59329:	gap of unknown length	gap	/estimated_length=unknown
* 59330	60889:	contig of 1560 bp in length	gap	67581..67680
* 60890	60989:	gap of unknown length	gap	/estimated_length=unknown
* 65147	contig of 4158 bp in length	gap	gap	68777..68876
* 65247	gap of unknown length	gap	gap	/estimated_length=unknown
* 65248	67580:	contig of 2333 bp in length	gap	85494..85593
* 67581	67680:	gap of unknown length	gap	/estimated_length=unknown
* 67681	68776:	contig of 1096 bp in length	gap	90518..90617
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* 68877	85493:	contig of 16617 bp in length	gap	111501..111600
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* 85594	90517:	contig of 4924 bp in length	gap	112665..112764
* 90518	90617:	gap of unknown length	gap	/estimated_length=unknown
* 90618	111500:	contig of 20883 bp in length	gap	122910..123009
* 111501	111600:	gap of unknown length	gap	/estimated_length=unknown
* 111601	112664:	contig of 1064 bp in length	gap	127131..127230
* 112665	112764:	gap of unknown length	gap	/estimated_length=unknown
* 112765	122909:	contig of 10145 bp in length	gap	130720..130819
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* 127231	127230:	gap of unknown length	gap	162844..162943
* 130719	contig of 3489 bp in length	gap	gap	167187..167286
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* 130820	140093:	contig of 9274 bp in length	gap	169931..170030
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* 140194	162843:	contig of 22650 bp in length	gap	175432..175531
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* 167187	167286:	gap of unknown length	gap	/estimated_length=unknown
* 167287	169930:	contig of 2644 bp in length	gap	178664..178763
* 169931	170030:	gap of unknown length	gap	/estimated_length=unknown
* 170031	175431:	contig of 5401 bp in length	gap	182004..182004
* 175432	175531:	gap of unknown length	gap	9.24; Score 76; DB 14; Length 182004;
* 175532	177305:	contig of 1774 bp in length	gap	Query Match
* 177306	177405:	gap of unknown length	gap	Best Local Similarity 100.0%; Pred. No. 5.3e-34;
* 177406	178663:	contig of 1258 bp in length	gap	Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
* 178664	178763:	gap of unknown length	gap	
* 178764	182004:	contig of 3241 bp in length.	gap	
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Best Local Similarity 100.0%; Pred. No. 5.3e-34;				
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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QY	243	CCATTGTACATGCCCT 258		
Db	47516	CCATTGTACATGCCCT 47531		
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WPCOMMENT				
Sequence split into 4 fragments LOCUS AY664417 Accession AY664417				
Fragment Name				
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AY664417_1				
AY664417_2				
AY664417_3				

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gap	158246. .158345	/estimated_length=unknown	
gap	159779. .159878	/estimated_length=unknown	
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Matches			61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	143	CGAATATAGAGCTAAGACACTGCTTCGTCAGATACATGCTCTTGAGATTTTACAT	202
Db	192227	CGAATATAGAGCTAAGACACTGCTTCGTCAGATACATGCTCTTGAGATTTTACAT	192286

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* 80003 82646: contig of 2644 bp in length
* 82647 82746: gap of unknown length
* 82747 98869: contig of 16123 bp in length
* 98870 98969: gap of unknown length
* 98970 102329: contig of 3360 bp in length
* 102330 102430: gap of unknown length
* 102430 105931: contig of 3502 bp in length
* 105931 106031: gap of unknown length
* 106031 124298: contig of 18267 bp in length
* 124298 124398: gap of unknown length
* 124398 125779: contig of 1181 bp in length
* 125779 125880: gap of unknown length
* 125880 130751: contig of 5072 bp in length
* 130751 130851: gap of unknown length
* 130851 144420: contig of 13569 bp in length
* 144420 144520: gap of unknown length
* 144520 148120: contig of 3600 bp in length.
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    /strain="B73"
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FEATURES

source

ORIGIN

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Query Match      6.1%; Score 50; DB 14; Length 148120;
Best Local Similarity 100.0%; Pred. No. 5e-18;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8

AC149836

LOCUS

DEFINITION

Zea mays clone ZMMBCC0496L17, *** SEQUENCING IN PROGRESS ***, 2

ordered pieces.

ACCESSION

AC149836

VERSION

AC149836.2 GI:57790161

KEYWORDS

HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.

SOURCE

Zea mays

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K. and Messing,J.

Zea mays, clone ZMMBCC0496L17

TITLE

JOURNAL

2 (bases 1 to 112468)

REFERENCE

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K., Messing,J., Abouelleil,A., Allen,N., Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukigalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R., Maclean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Melidrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

Direct Submission

REFERENCE

AUTHORS

Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

TITLE

JOURNAL

3 (bases 1 to 112468)

REFERENCE

AUTHORS

Birren,B., Nusbaum,C., Lander,E., Butler,E., Wing,R., Bharti,A.K., Messing,J., Abouelleil,A., Allen,N., Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T., Boguslavskiy,L., Boukigalter,B., Camarata,J., Chang,J., Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B., Dearellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kanat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R., Maclean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Melidrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE

JOURNAL

Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

AUTHORS

Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

TITLE

JOURNAL

Submitted (103-FEB-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

AUTHORS

On Jan 14, 2005 this sequence version replaced gi:49035067.

TITLE

JOURNAL

All repeats were identified using RepeatMasker:

REFERENCE

AUTHORS

Smith, A.F.A. & Green, P. (1996-1997)

TITLE

JOURNAL

http://ftp.genome.washington.edu/RM/RepeatMasker.html

REFERENCE

AUTHORS

Center: Broad Institute of MIT and Harvard

TITLE

JOURNAL

Center code: WIBR

REFERENCE

AUTHORS

Web site: http://www-seq.wi.mit.edu

TITLE

JOURNAL

Contact: sequence_submissions@broad.mit.edu

REFERENCE

AUTHORS

Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA

TITLE

JOURNAL

(http://pgir.rutgers.edu)

REFERENCE

AUTHORS

Butler, E and Wing, R: Arizona Genomics Institute, Biological

Sciences West, 448A, P.O. Box 210088, University of Arizona,
Tucson, AZ 85721, USA (<http://www.genome.arizona.edu>)
----- Project Information
Center Project name: L30352
Center clone name: 496_L_17

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 62677: contig of 62677 bp in length
* 62678 112468: contig of unknown length
* 62778 112468: contig of 49691 bp in length.

FEATURES

Location/Qualifiers
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ORIGIN

Query Match 5.6%; Score 46; DB 14; Length 112468;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACGGTACTCCAGTATAGACACACGCTAAACACACATAT 46
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DB 2368 CTGACGGTACTCCAGTATAGACACACGCTAAACACACATAT 2413

RESULT 9
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LOCUS AC149827 143793 bp DNA linear HTG 03-FEB-2005
DEFINITION Zea mays clone ZM5B0051H21, *** SEQUENCING IN PROGRESS ***, 8
unordered pieces.

AC149827
AC149827 GI:57790148
HTG: HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEPIN.

SOURCE

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 143793)
Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.
and Messing, J.

Zea mays, clone ZM5B0051H21
Unpublished

2 (bases 1 to 143793)

Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.,
Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,
Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Corum, B., DeArelano, K., Diaz, J.S., Dodge, S.,
Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P.,
Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L.,
Grand-pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P.,
Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Roman, J., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission

TITLE

JOURNAL

REFERENCE

AUTHORS

Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 143793)
Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.,
Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,
Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Corum, B., DeArelano, K., Diaz, J.S., Dodge, S.,
Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P.,
Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L.,
Grand-pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
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Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
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Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (03-FEB-2005) Broad Institute of MIT and Harvard, 320
Charles Street, Cambridge, MA 02141, USA
On Jan 14, 2005 this sequence version replaced gi:49035053.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
----- Genome Center
Center: Broad Institute of MIT and Harvard
Center code: W1BR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@broad.mit.edu

Center: Broad Institute of MIT and Harvard

Center code: W1BR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@broad.mit.edu

Bharti, AK and Messing, J: The Plant Genome Initiative at
Rutgers, Waksman Institute, Rutgers, The State University of New
Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
(<http://pgir.rutgers.edu>)

Butler, E and Wing, R: Arizona Genomics Institute, Biological
Sciences West, 448A, P.O. Box 210088, University of Arizona,
Tucson, AZ 85721, USA (<http://www.genome.arizona.edu>)

----- Project Information

Center Project name: L30279

Center clone name: 51_H_21

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 30907: contig of 30907 bp in length
* 30908 30007: gap of unknown length
* 31008 36273: contig of 5266 bp in length
* 36274 36373: gap of unknown length
* 36374 45682: contig of 9209 bp in length
* 45683 45682: gap of unknown length
* 45683 78484: contig of 32802 bp in length
* 78485 78584: gap of unknown length
* 78585 98756: contig of 21172 bp in length
* 98757 98856: gap of unknown length
* 98857 120940: contig of 21084 bp in length

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 /translation="MSDRKMSQWQYVDEHLMCELEGHLLAAALVGHGDAWAQSTA
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 93.95
 /note="2nd start codon; in-frame"

misc_feature

ORIGIN

Query Match 4.6%; Score 38; DB 15; Length 830;
 Best Local Similarity 100.0%; Pred. No. 8.5e-11;
 Matches. 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 786 CCTCTCCCTCCCTCCGATCCATTCCTCCAGCGCAG 823

DB 27 CCTCTCCCTCCCTCCGATCCATTCCTCCAGCGCAG 64

RESULT 12

AC145389 198102 bp DNA linear HTG 20-JUN-2004
 LOCUS Zea mays clone ZM5B0054A01, *** SEQUENCING IN PROGRESS ***, 4
 DEFINITION ordered pieces.

ACCESSION AC145389

VERSION AC145389.6 GI:48762556

KEYWORDS HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 198102)
 Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.
 and Messing, J.

Zea mays, clone ZM5B0054A01

2 (bases 1 to 198102)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
 Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
 Boguslavsky, L., Bouknight, B., Camarata, J., Chang, J., Choepel, Y.,
 Collymore, A., Cook, A., Cooke, P., Corum, B., DeArelano, K.,
 Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
 Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,
 Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
 Hall, J., Karatas, A., Kells, C., Landers, T., Levine, R.,
 Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
 Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C.,
 Macdonald, P., Major, J., Manning, J., Meng, V., Matthews, C., McCarthy, M.,
 Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
 Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
 Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
 Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
 Talamas, J., Teefave, S., Theodore, J., Topham, K., Travers, M.,
 Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
 Submitted (01-JUL-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 198102)
 Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.,
 Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,
 Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
 Bouknight, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,
 Cook, A., Cooke, P., Corum, B., DeArelano, K., Diaz, J.S., Dodge, S.,
 Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P.,
 Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L.,
 Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J.,
 Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
 Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P.,
 Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J.,
 Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,

TITLE

JOURNAL

REFERENCE

AUTHORS

FEATURES

source

1. 198102
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone="ZM5B0054A01"
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Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
 Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
 Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
 Talamas, J., Teefave, S., Theodore, J., Topham, K., Travers, M.,
 Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (20-JUN-2004) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jun 16, 2004 this sequence version replaced gi:48717652.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@broad.mit.edu

Bharti, AK and Messing, J.: The Plant Genome Initiative at
 Rutgers, Waksman Institute, Rutgers, The State University of New
 Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 (http://pgir.rutgers.edu)

Butler, E and Wing, R.: Arizona Genomics Institute, Biological
 Sciences West, 448A, P.O. Box 210088, University of Arizona,
 Tucson, AZ 85721, USA (http://www.genome.arizona.edu)

----- Project Information

Center Project name: L29613

Center Clone name: 54_A_1

----- Consensus Information

This consensus is derived from a shotgun assembly that has been
 manually curated. It is the best representation of the BAC that we
 can generate without further laboratory work. The draft assembly
 has been edited, and if possible, ends identified by vector as well
 as by BAC end sequences, and contigs ordered and oriented. This
 assembly was performed with Phrap. All trace files for this project
 are available at the NCBI trace repository
 (http://www.ncbi.nlm.nih.gov/Traces/trace.cgi?). An exact list of
 reads used in this assembly are available at
 http://www.broad.mit.edu/annotation/plants/maize/randomclones.html.

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 20266: contig of 20266 bp in length
 * 20267 20366: gap of 100 bp
 * 20367 78634: contig of 58268 bp in length
 * 78635 78734: gap of 100 bp
 * 78735 140318: contig of 61584 bp in length
 * 140319 140418: gap of 100 bp
 * 140419 198102: contig of 57684 bp in length.

Location/Qualifiers

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 /estimated_length=100
 78635 - 78734
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 140319 - 140418

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Best Local Similarity 100.0%; Pred. No. 4.9e-10;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 CAATCAGAACATTCATTAATAAATGACCAATCAG 128
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RESULT 13
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LOCUS ZMGLOSSY 6343 bp DNA linear PLN 09-MAY-1996
DEFINITION Z.mays Glossy2 locus DNA.
ACCESSION X88779
VERSION X88779.1 GI:949979
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1
AUTHORS Tacke, E., Korfthage, C., Michel, D., Maddaloni, M., Motto, M.,
Lanzini, S., Salamini, F. and Doring, H.P.
TITLE Transposon tagging of the maize Glossy2 locus with the transposable
element En/Spm
JOURNAL Plant J. 8 (6), 907-917 (1995)
PUBMED 8580961
REFERENCE 2
AUTHORS Tacke, E.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-1995) E. Tacke, Max-Planck-Institute, Dept.
Salamini, Carl-von-Linne-Weg 10, 50829 Koeln, NRW, FRG
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LALGFWAHLGIDTPSAATCFNKWAILSGKKPEATVLTTPNPLQGSPPAPRSVKQ
VGPTEDLVLPAGDMACYSFHVSDAVLKKLHQOQNGRQDAAGTFFELVSLVQVAV
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intron
exon

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QY 101 CATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 136
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DB 3715 CATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 3750

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RESULT 14
LOCUS AC149816/c
DEFINITION Zea mays clone ZM5BB0309E13, *** SEQUENCING IN PROGRESS ***, 7
unordered pieces.
ACCESSION AC149816
VERSION AC149816.2 GI:57790137
KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1
AUTHORS Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.
and Messing, J.
TITLE Zea mays, clone ZM5BB0309E13
JOURNAL Unpublished
REFERENCE 2
AUTHORS (bases 1 to 69497)
Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,
Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S.,
Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P.,
FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L.,
Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A.,
Karakas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P.,
Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talanas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, W.
Direct Submission
JOURNAL Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3
AUTHORS (bases 1 to 69497)
Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.,
Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,
Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S.,
Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P.,
FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L.,
Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A.,
Karakas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P.,
Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
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Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, W.
Direct Submission
JOURNAL Submitted (03-FEB-2005) Broad Institute of MIT and Harvard, 320
Charles Street, Cambridge, MA 02141, USA

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COMMENT
On Jan 14, 2005 this sequence version replaced gi:49035040.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Broad Institute of MIT and Harvard
Center code: W1BR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu
-----
Bharti, AK and Messing, J: The Plant Genome Initiative at
Rutgers, Waksman Institute, Rutgers, The State University of New
Jersey, 150 Frelinghuysen Road, Piscataway, NJ 08854, USA
(http://pgir.rutgers.edu)
Butler, E and Wing, R: Arizona Genomics Institute, Biological
Sciences West, 448A, P.O. Box 210088, University of Arizona,
Tucson, AZ 85721, USA (http://www.genome.arizona.edu)
----- Project Information
Center project name: L20238
Center clone name: 309_E_13
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 2922: contig of 2922 bp in length
* 2923 3022: gap of unknown length
* 3023 15817: contig of 12795 bp in length
* 15818 15917: gap of unknown length
* 15918 25218: contig of 9301 bp in length
* 25219 25318: gap of unknown length
* 25319 42542: contig of 17224 bp in length
* 42543 42642: gap of unknown length
* 42643 45994: contig of 3352 bp in length
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* 46095 68616: contig of 22522 bp in length
* 68617 68716: gap of unknown length
* 68717 69497: contig of 781 bp in length.
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* Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 32782 CCCCCTAGACACACTCTTAAGACACACACTTAAAGACAC 32747
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AF348367/c
LOCUS AF348367 1257 bp DNA linear PLN 02-MAR-2002
DEFINITION Zea mays inbred B77 beta-keto acyl reductase gene, partial cds.
ACCESSION AF348367
VERSION AF348367.1 GI:19070512
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1257)
AUTHORS Dietrich,C.R., Cui,F., Packila,M.L., Li,J., Ashlock,D.A.,
Nikolau,B.J. and Schnable,P.S.
TITLE Maize Mu transposons are targeted to the 5' untranslated region of
the g18 gene and sequences flanking Mu target-site duplications
exhibit nonrandom nucleotide composition throughout the genome
Genetics 160 (2), 697-716 (2002)
JOURNAL 11861572
PUBMED 11861572
REFERENCE 2 (bases 1 to 1257)
AUTHORS Dietrich,C.R., Packila,M.L., Li,J., Ashlock,D.A., Nikolau,B.J. and
Schnable,P.S.
TITLE Direct Submission
JOURNAL Submitted (12-FEB-2001) Zoology and Genetics, Iowa State
University, B420 Agronomy Hall, Ames, IA 50011, USA
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Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 324 ATTCAATAAATTAAGTGACCAATCAGATAGTCTC 290
Search completed: March 5, 2006, 12:38:18
Job time : 4265 secs
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